

Thu Apr 29 08:44:17 2004

us-10-669-689-1.rnpb

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2004, 16:16:37 ; Search time 1217 Seconds

(without alignments)
11573.501 Million cell updates/sec

Title: US-10-669-689-1

Perfect score: 3124
Sequence: 1 tccgccccgccccggggtg.....aaaaaaaaaaaaaaaa 3124

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgnt_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
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18: /cgnt_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgnt_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3124	100.0	3124	US-10-669-689-1	Sequence 1, Appli
2	3124	100.0	3124	US-10-153-921-1	Sequence 1, Appli
3	3000.8	96.1	3017	US-10-258-106-35	Sequence 35, Appli
4	2791.2	89.3	2840	US-10-037-270-20	Sequence 20, Appli
5	2791.2	89.3	2840	US-10-117-722-20	Sequence 20, Appli
6	2780.8	88.0	2895	US-10-425-114-26867	Sequence 26867, A
7	2773.8	88.8	2880	US-10-425-114-26849	Sequence 26849, A
8	2709.2	86.7	3236	US-10-425-114-26858	Sequence 26858, A
9	2595.2	83.1	2747	US-10-037-270-19	Sequence 19, Appli
10	2595.2	83.1	2747	US-10-117-722-19	Sequence 19, Appli
11	2283.4	73.1	2297	US-09-797-039-1	Sequence 1, Appli
12	2283.4	73.1	2297	US-10-423-543-18	Sequence 18, Appli
13	2283.4	73.1	2297	US-10-170-789-1	Sequence 1, Appli
14	1876.6	60.1	3915	US-09-764-868-1378	Sequence 1378, Ap

15	1876.6	60.1	7542	13	US-10-669-689-3	Sequence 3, Appli
16	1876.6	60.1	7542	13	US-10-153-921-3	Sequence 3, Appli
17	1617	51.8	1703	16	US-10-085-198-5	Sequence 5, Appli
18	1504.4	48.2	1506	13	US-10-423-543-20	Sequence 20, Appli
19	1501.4	48.1	1503	9	US-09-797-039-3	Sequence 3, Appli
20	1501.4	48.1	1503	15	US-10-170-789-3	Sequence 3, Appli
21	936.4	30.0	1069	15	US-09-933-767-74	Sequence 74, Appli
22	936.4	30.0	1069	13	US-10-004-860-74	Sequence 74, Appli
23	936.4	30.0	1069	15	US-10-023-282-74	Sequence 74, Appli
24	850	27.2	862	13	US-09-823-245-520	Sequence 520, Appli
25	593.6	19.0	727	11	US-09-764-875-127	Sequence 127, Appli
26	497.8	15.9	658	9	US-09-764-868-219	Sequence 219, Appli
27	497.8	15.9	658	11	US-09-764-875-437	Sequence 437, Appli
28	464	14.9	544	13	US-10-296-115-22	Sequence 22, Appli
29	412.4	13.2	460	10	US-09-918-995-1367	Sequence 1367, Appli
30	265.8	8.5	1480	15	US-10-204-041-9	Sequence 9, Appli
31	265.8	8.5	1480	16	US-10-305-720-1454	Sequence 1454, Appli
32	258	8.3	264	16	US-10-305-720-543	Sequence 543, Appli
33	254.8	8.2	1452	13	US-10-425-114-26649	Sequence 26649, A
34	252.6	8.1	1584	13	US-10-302-172-205	Sequence 205, Appli
35	249.2	8.0	1694	15	US-10-355-975-3	Sequence 3, Appli
36	249	8.0	1458	10	US-09-735-138-5	Sequence 5, Appli
37	244.8	7.8	1651	16	US-10-258-106-29	Sequence 29, Appli
38	244.8	7.8	1733	15	US-10-037-270-526	Sequence 526, Appli
39	244.8	7.8	1733	16	US-10-117-722-526	Sequence 526, Appli
40	244.8	7.8	1736	16	US-10-258-106-20	Sequence 20, Appli
41	244.8	7.8	1772	15	US-10-024-036B-1	Sequence 1, Appli
42	243.6	7.8	1383	10	US-09-935-64-2	Sequence 2, Appli
43	243.6	7.8	1383	15	US-10-125-835-2	Sequence 2, Appli
44	243.6	7.8	1738	10	US-09-935-64-4	Sequence 4, Appli
45	243.6	7.8	1738	15	US-10-125-835-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-669-689-1
; Sequence 1, Application US/10669689
; Publication No. US2004003863A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00612DIVIT
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2000-12-12
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-689-1
Query Match 100.0%; Score 3124; DB 13; Length 3124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGCCCGCGCGCGGCTGCGAATCCGCTCCGCGCAAGCGAGCTGCGATGCTGAGGTT 60
DB 1 TCCGCCCGCGCGCGGCTGCGAATCCGCTCCGCGCAAGCGAGCTGCGATGCGAGGTT 60
QY 61 CCGTAGCCGAGAGCGGCTGCTGCGCGCGGCTGCGCGCGGCTGCGAGCGGATTTCT 120
DB 61 CCGTAGCCGAGAGCGGCTGCTGCGCGCGGCTGCGCGCGGCTGCGAGCGGATTTCT 120
QY 121 GCCCGCGTCCCGGAGCGCTGCGCGCGCGCGCGCTGAGCCCGGATCACTTCCCTGTGA 180
DB 121 GCCCGCGTCCCGGAGCGCTGCGCGCGCGCGCGCTGAGCCCGGATCACTTCCCTGTGA 180

[illegible]

Db	1201	CAATCCAGCAGCGCTGACGCCCAAGTCGGGCTCAGGCCACAGAACACTGCGCACCCCCGGGGGCT	1260
Qy	1261	GCAGGTGGGGCCCAAGCTCAGCTGCGAGTGGAGTACTTCAAGCCCTGAGGGGTATGCT	1320
Db	1261	GCAGGTGGGGCCCAAGCTCAGCTGCGAGTGGAGTACTTCAAGCCCTGAGGGGTATGCT	1320
Qy	1321	GCTCTGCTGCAAAAGAGTGAATAATGAGGCCCGCCGCGAGACCGTAAGTGGCCCCCAGCACCA	1380
Db	1321	GCTCTGCTGCAAAAGAGTGAATAATGAGGCCCGCCGCGAGACCGTAAGTGGCCCCCAGCACCA	1380
Qy	1381	GATGGAAAGTGCACCCCGACGCACTGATGGCAGTGTACCCCGACGCCACCCAGTAAAGCATC	1440
Db	1381	GATGGAAAGTGCACCCCGACGCACTGATGGCAGTGTACCCCGACGCCACCCAGTAAAGCATC	1440
Qy	1441	ACTCCAGCCCATGATGGAGTGTACCCCGATCATCTGAACGAGCGCTTACTCCAGCATT	1500
Db	1441	ACTCCAGCCCATGATGGAGTGTACCCCGATCATCTGAACGAGCGCTTACTCCAGCATT	1500
Qy	1501	GATGGAGAGCCACACCAAGCCACAGAAAGACACTGTGCCACCCACCCAGCAAGAGTGGC	1560
Db	1501	GATGGAGAGCCACACCAAGCCACAGAAAGACACTGTGCCACCCACCCAGCAAGAGTGGC	1560
Qy	1561	ATGTGGCCCAACAAAGGAGCTGGCAACCCCTGAGCCGAGTATGGCCCGACCGGACACACA	1620
Db	1561	ATGTGGCCCAACAAAGGAGCTGGCAACCCCTGAGCCGAGTATGGCCCGACCGGACACACA	1620
Qy	1621	GCCCCAGAGGGCGCCACAGGCCAGGCTCCACCCCTTAATGAAGGGAAGAGGTCTGGT	1680
Db	1621	GCCCCAGAGGGCGCCACAGGCCAGGCTCCACCCCTTAATGAAGGGAAGAGGTCTGGT	1680
Qy	1681	TATGCCCAAGAGTCTCAAAGGAGAGAGCCAGCTGATAGGAGCCGTGGTGAAGGGGGGGC	1740
Db	1681	TATGCCCAAGAGTCTCAAAGGAGAGAGCCAGCTGATAGGAGCCGTGGTGAAGGGGGGGC	1740
Qy	1741	AGGGGAATGGGAGAGGAGGTGGAGAGATGAAGGGGCTTCTCACTGTATCATATGAGTCAAC	1800
Db	1741	AGGGGAATGGGAGAGGAGGTGGAGAGATGAAGGGGCTTCTCACTGTATCATATGAGTCAAC	1800
Qy	1801	TGGCATGATGCGCTCGCTCCGCCATGCCCCACATCCCAAGTGGGGCATTAATGAGGGGTCA	1860
Db	1801	TGGCATGATGCGCTCGCTCCGCCATGCCCCACATCCCAAGTGGGGCATTAATGAGGGGTCA	1860
Qy	1861	CGGGAGAGCAATCTCTGCTCTCTGTGTATGTGTGTAGTGTGTGGAGAGGCCAGTGGCAG	1920
Db	1861	CGGGAGAGCAATCTCTGCTCTCTGTGTATGTGTGTAGTGTGTGGAGAGGCCAGTGGCAG	1920
Qy	1921	GCGGAGAGCAATCTCTGCTCTCTGTGTATGTGTGTAGTGTGTGGAGAGGCCAGTGGCAG	1980
Db	1921	GCGGAGAGCAATCTCTGCTCTCTGTGTATGTGTGTAGTGTGTGGAGAGGCCAGTGGCAG	1980
Qy	1981	AGTTTCTGTTCTTGTGGATGCTCTTAAGGATACTCAGGGGGCTCTGCTCTCTTC	2040
Db	1981	AGTTTCTGTTCTTGTGGATGCTCTTAAGGATACTCAGGGGGCTCTGCTCTCTTC	2040
Qy	2041	CCCTTCCCTTCTTGTGCTTACCATTCCTCCCTTAGGCAAGGCCCTGCAAGTCCCACTCTCCCA	2100
Db	2041	CCCTTCCCTTCTTGTGCTTACCATTCCTCCCTTAGGCAAGGCCCTGCAAGTCCCACTCTCCCA	2100
Qy	2101	GCGCCCTTAACCTGGGCGGCTTGGCCCTGAGAGCTGTGCTTCCAGCGAGGCCCTGTCAAGC	2160
Db	2101	GCGCCCTTAACCTGGGCGGCTTGGCCCTGAGAGCTGTGCTTCCAGCGAGGCCCTGTCAAGC	2160
Qy	2161	GCTTAGGCTCCTGACATGAAGGTGTGTGCTGTGAGTGGCTTCTTAGAGCAG	2220
Db	2161	GCTTAGGCTCCTGACATGAAGGTGTGTGCTGTGAGTGGCTTCTTAGAGCAG	2220
Qy	2221	ATACAGGCTGTATATGAGAGATGCAGAAAGTATGGGCAATGTTTAAGTCCAGCTTGGC	2280
Db	2221	ATACAGGCTGTATATGAGAGATGCAGAAAGTATGGGCAATGTTTAAGTCCAGCTTGGC	2280
Qy	2281	AATAGGCTAAGGATATGCTGCTACATAGCTGTGGAAGTCTCTCAGAGTGGAGAGATATGATTA	2340
Db	2281	AATAGGCTAAGGATATGCTGCTACATAGCTGTGGAAGTCTCTCAGAGTGGAGAGATATGATTA	2340

QY 2341 GGAGGAGAGAGCTTCATTTTGTCTCTCTAAGACCTGTATTTGTATTTCTG 2400
DB 2341 GGAGGAGAGAGCTTCATTTTGTCTCTCTAAGACCTGTATTTGTATTTCTG 2400
QY 2401 CCTTCCGAGTCTGCACTGAGGCTGCTTACCTGAACTCATAGGCTCTAAGGAA 2460
DB 2401 CCTTCCGAGTCTGCACTGAGGCTGCTTACCTGAACTCATAGGCTCTAAGGAA 2460
QY 2461 AGAGAGAAATTAAGACCTGCAATAGACCTGCAAGGCAAGTAAAGCCACACAC 2520
DB 2461 AGAGAGAAATTAAGACCTGCAATAGACCTGCAAGGCAAGTAAAGCCACACAC 2520
QY 2521 CAGTGTCCGAGCTTATGAGGCTCTTACCTGAGGCAAGGAGGAGTATCTCT 2580
DB 2521 CAGTGTCCGAGCTTATGAGGCTCTTACCTGAGGCAAGGAGGAGTATCTCT 2580
QY 2581 TGCTCTCTAGATGAGGCTCTTACCTGCAATCTGAGCCCAAGTCTTCCACCTAAGG 2640
DB 2581 TGCTCTCTAGATGAGGCTCTTACCTGCAATCTGAGCCCAAGTCTTCCACCTAAGG 2640
QY 2641 GGCTTCTGATGAGCAATTAATCTAATCTGATTTGAGGTTGCTTTACAGGAGCAG 2700
DB 2641 GGCTTCTGATGAGCAATTAATCTAATCTGATTTGAGGTTGCTTTACAGGAGCAG 2700
QY 2701 ATTTTCTGCTCAGTTCAACATGAATGAAGAGAACTCCCTCTTCTAAGCTCACTTC 2760
DB 2701 ATTTTCTGCTCAGTTCAACATGAATGAAGAGAACTCCCTCTTCTAAGCTCACTTC 2760
QY 2761 TATCAGAGGAGGAGGCTCTCAGAGCCACATTTGATTTGTTTCTGAGATGAGAGTA 2820
DB 2761 TATCAGAGGAGGAGGCTCTCAGAGCCACATTTGATTTGTTTCTGAGATGAGAGTA 2820
QY 2821 GGGTTAAACTCCCAAGTTTCTGAGGAGGCTCTGAGAGGCTCTTCTGAGAGCTTA 2880
DB 2821 GGGTTAAACTCCCAAGTTTCTGAGGAGGCTCTGAGAGGCTCTTCTGAGAGCTTA 2880
QY 2881 CCAAGAGCTGATAGGAGGCACTTGTCTCTGAGGCTCTGAGGCTCTTCTGAGAGCTTA 2940
DB 2881 CCAAGAGCTGATAGGAGGCACTTGTCTCTGAGGCTCTGAGGCTCTTCTGAGAGCTTA 2940
QY 2941 CTGAGCTTCTGAGGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTTCTGAGAGCTTA 3000
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QY 3001 TGCTGCTCTGAGGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTTCTGAGAGCTTA 3060
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QY 3061 AAAAAAATTAAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTTCTGAGAGCTTA 3120
DB 3061 AAAAAAATTAAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTTCTGAGAGCTTA 3120
QY 3121 AAAAA 3124
DB 3121 AAAAA 3124

RESULT 2

US-10-153-921-1

Sequence 1, Application US/10153921

Publication No. US20020142430A1

GENERAL INFORMATION:

APPLICANT: YAN Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: CLO00612D1V

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: 60/207,281

PRIOR FILING DATE: 2000-05-30

PRIOR APPLICATION NUMBER: 09/734,030

;; PRIOR FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 3124
;; TYPE: DNA
;; ORGANISM: HOMO SAPIEN
US-10-153-921-1

Query Match 100.0%; Score 3124; DB 14; Length 3124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCCCCGGCGGAGGCTGCAATCCGAGTCCGCAAGCGGCTGCGATGCTGAGGTT 60
DB 1 TCCGCCCCCGGCGGAGGCTGCAATCCGAGTCCGCAAGCGGCTGCGATGCTGAGGTT 60
QY 61 CGCTAGCCGAAAGCGGCTGCAATCTGAGCGCGGCTGCTGCGCGCGGCTGCGAGGATTTCT 120
DB 61 CGCTAGCCGAAAGCGGCTGCAATCTGAGCGCGGCTGCTGCGCGCGGCTGCGAGGATTTCT 120
QY 121 GCGCGCGGCTGCGGAGCGCTGCGCGCGGCTGAGCGCGGATCACTTCTCCCTGGA 180
DB 121 GCGCGCGGCTGCGGAGCGCTGCGCGCGGCTGAGCGCGGATCACTTCTCCCTGGA 180
QY 181 CCAACCGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 240
DB 181 CCAACCGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 240
QY 241 AAGAAATTAATTAACCAAGCCATCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 300
DB 241 AAGAAATTAATTAACCAAGCCATCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 300
QY 301 AAGCTGAGAGGTTTGTGAATCTTCCGCGCAAGGCAAGACGAGGCTGAGGCTGAG 360
DB 301 AAGCTGAGAGGTTTGTGAATCTTCCGCGCAAGGCAAGACGAGGCTGAGGCTGAG 360
QY 361 ACCGCAAGGATTCAGAGGCGGAGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGG 420
DB 361 ACCGCAAGGATTCAGAGGCGGAGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGG 420
QY 421 ATAGCATCTCAAGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
DB 421 ATAGCATCTCAAGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 480
QY 481 ACCGCAAGGATTCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 540
DB 481 ACCGCAAGGATTCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 540
QY 541 ATCTGAGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 600
DB 541 ATCTGAGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 600
QY 601 GAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 660
DB 601 GAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 660
QY 661 CTGCTTACTCAACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
DB 661 CTGCTTACTCAACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 720
QY 721 AAGCTGAAATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 780
DB 721 AAGCTGAAATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 780
QY 781 GGTGTGCGGCGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 840
DB 781 GGTGTGCGGCGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 840
QY 841 TACATCTGCTTCAAGCAATCACTTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAG 900
DB 841 TACATCTGCTTCAAGCAATCACTTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAG 900

QY	1293	AGCTACCTCAGCCCTCAGGAGGTGATGTGCTCGCTGCAAAAGTATATATGTGGCCCC	1352
Dp	1262	AGTACTCTCAGCCCTTAGGGGTATGTCTGCTCGCTGCAAAAGTATATATGTGGCCCC	1321
QY	1353	CGCAGACCGTATGTGCACCCCGCACAGATGGAAAGTGTCCACCCCGCACCTGATGCGAG	1412
Dp	1322	CGCAGACCGTATGTGCACCCCGCACAGATGGAAAGTGTCCACCCCGCACCTGATGCGAG	1381
QY	1413	TGTACCCCCCAGCCCGCATGGAAAGTACTTCCAGCCACTGATGGAGTGTACCCCACT	1472
Dp	1382	TGTACCCCCCAGCCCGCATGGAAAGTACTTCCAGCCACTGATGGAGTGTACCCCACT	1441
QY	1473	CACCTGACAGAGCGGCTACTCCAGCCACTGATGGAGAGCCACACACCCACAGAAAGAG	1532
Dp	1442	CACCTGACAGAGCGGCTACTCCAGCCACTGATGGAGAGCCACACACCCACAGAAAGAG	1501
QY	1533	CACGTGTCCCAACCAACCAAGCAATGTGCATGTCTGCGCACCAAGGCAAGTCCACCCCTGA	1592
Dp	1502	CACGTGTCCCAACCAACCAAGCAATGTGCATGTCTGCGCACCAAGGCAAGTCCACCCCTGA	1561
QY	1593	GCCGGCTATGCGCCCGGACCGGACAGCACAGCCCGCAGAGGCGCCACAGGCGCAAGCTCCACC	1652
Dp	1562	GCCGGCTATGCGCCCGGACCGGACAGCACAGCCCGCAGAGGCGCCACAGGCGCTCCACC	1621
QY	1653	CTCTAGTAAAGGGGAAAGAGCTGCTGTGTATGTGCCAAGATCTTAAAGGGAGAGGCTCAG	1712
Dp	1622	CTCTAGTAAAGGGGAAAGAGCTGCTGTGTATGTGCCAAGATCTTAAAGGGAGAGGCTCAG	1681
QY	1713	CTGAGTATAGGCGAGCTGGTGAAGGGGGGCGAGGGGATGGGCGAGAGAGGATGGATG	1772
Dp	1682	CTGAGTATAGGCGAGCTGGTGAAGGGGGGCGAGGGGATGGGCGAGAGGATGGATG	1741
QY	1773	AGGGGCTTCTCACTGTACATAGACTCACTGGCAATGATGCCCCCTGCCATGCCCA	1832
Dp	1742	AGGGGCTTCTCACTGTACATAGACTCACTGGCAATGATGCCCCCTGCCATGCCCA	1801
QY	1833	CATCCCAATGGGGCAATTAATGAGGATCAAGGGAAGACAGTCTCTCTGTGTGTATGT	1892
Dp	1802	CATCCCAATGGGGCAATTAATGAGGATCAAGGGAAGACAGTCTCTCTGTGTGTATGT	1861
QY	1893	GTGTGAGTGTGTGGGACAGGCGACAGTGGCGAGGGCGGGCCCGACGCCCTGATGATTCCTGT	1952
Dp	1862	GTGTGAGTGTGTGGGACAGGCGACAGTGGCGAGGGCGGGCCCGACGCCCTGATGATTCCTGT	1921
QY	1953	GGCTTTTCTGTCTTTGTAGACTTCAACAGATTTCTGTCTCTGTGGAGTGTGCTTAGG	2012
Dp	1922	GGCTTTTCTGTCTTTGTAGACTTCAACAGATTTCTGTCTCTGTGGAGTGTGCTTAGG	1981
QY	2013	GATACTCAGGGGGCTCTGTCTCTCTTCCCTTCCCTTCTTGCCTCACATTCCTCAGG	2072
Dp	1982	GATACTCAGGGGGCTCTGTCTCTCTTCCCTTCCCTTCCCTTCTTGCCTCACATTCCTCAGG	2041
QY	2073	CAGGCGCTTGCAGGTTCACACTCTTCCAGGCGCTTAAATTGGGCGGCGCTTGCCCTGAGAG	2132
Dp	2042	CAGGCGCTTGCAGGTTCACACTCTTCCAGGCGCTTAAATTGGGCGGCGCTTGCCCTGAGAG	2101
QY	2133	CTGTGCTTCCACAGCGGCGCTTGCAGGCGGTCTTAGGCTCTGCGCACATGAAGTGTGAGCC	2192
Dp	2102	CTGTGCTTCCACAGCGGCGCTTGCAGGCGGTCTTAGGCTCTGCGCACATGAAGTGTGAGCC	2161
QY	2193	TGTGTGTGTGGGCTGTCTTAGAGACATATCAGGCTGTATAGAGATGCAGAAAGGTA	2252
Dp	2162	TGTGTGTGTGGGCTGTCTTAGAGACATATCAGGCTGTATAGAGATGCAGAAAGGTA	2221
QY	2253	GGGCGATATGTTTAAATCCCAATTTGGCAATGCTTAGGGATATCTGCTCACTAGCTGTGG	2312
Dp	2222	GGGCGATATGTTTAAATCCCAATTTGGCAATGCTTAGGGATATCTGCTCACTAGCTGTGG	2281
QY	2313	AGGTCCTCAGAGTGTGAGATATGACTAGAGGGGAGAAAGCTTCATTTTGTCTCTCT	2372
Dp	2282	AGGTCCTCAGAGTGTGAGATATGACTAGAGGGGAGAAAGCTTCATTTTGTCTCTCT	2341

QY	2373	AAGAACCCTGTATTATTGTGTATTTCTTCGCTTTCCGAGTCCTCGAGTGGGAGTGGGCGCCCTGTGA	2432
Db	2342	AAGACCCTGTATTATTGTGTATTTCTTCGCTTTCCGAGTCCTCGAGTGGGAGTGGGCGCCCTGTGA	2401
QY	2433	CCCTGAACCTCAATGAGACCTCTTAAGGGAAAGAGAAACAATTAGACGTGGCAATGAGACC	2492
Db	2402	CCCTGAACCTCAATGAGACCTCTTAAGGGAAAGAGAAACAATTAGACGTGGCAATGAGACC	2461
QY	2493	TGGCAGGGCAGAGTACAGACCAGCACCAGCAGTGTGCCAGCCTTACTGSGTCTTAACCTTG	2552
Db	2462	TGGCAGGGCAGAGTACAGACCAGCACCAGCAGTGTGCCAGCCTTACTGSGTCTTAACCTTG	2521
QY	2553	GGCCAAACAGGAGGAGGCTATACCTTCCTGCTCTTCTCTGATAGTGCCTACTCTTAACACT	2612
Db	2522	GGCCAAACAGGAGGAGGCTATACCTTCCTGCTCTTCTCTGATAGTGCCTACTCTTAACACT	2581
QY	2613	CAGCCCAACAAGTCTCTCCACCCTAGGGGGGCTGTGCGCATGGCAATACTCAATCTGGA	2672
Db	2582	CAGCCCAACAAGTCTCTCCACCCTAGGGGGGCTGTGCGCATGGCAATACTCAATCTGGA	2641
QY	2673	TTTGGAGGTTTGCCCTTTACAGGGGAGATTTTCTGCTCACTTCAACATGAAATGAAGA	2732
Db	2642	TTTGGAGGTTTGCCCTTTACAGGGGAGATTTTCTGCTCACTTCAACATGAAATGAAGA	2701
QY	2733	GGAACCTCCTCTTTCTTCAACAGCTCACTTCTATCAGAGGCCAGGTGCTTCAGAGCCACTT	2792
Db	2702	GGAACCTCCTCCTTTCTTCAACAGCTCACTTCTATCAGAGGCCAGGTGCTTCAGAGCCACTT	2761
QY	2793	GAGTTGCTTTTCTGGAGTGAAGAAAGTAAAGGTAAATCCCAAGTTCTCTGAGGAGAGCT	2852
Db	2762	GAGTTGCTTTTCTGGAGTGAAGAAAGTAAAGGTAAATCCCAAGTTCTCTGAGGAGAGCT	2821
QY	2853	CCTGACAGGAGCCCTTTGTCAGACCTTACACACAGCCTGGATAGAGCAGCCACTTGGTCTCT	2912
Db	2822	CCTGACAGGAGCCCTTTGTCAGACCTTACACACAGCCTGGATAGAGCAGCCACTTGGTCTCT	2881
QY	2913	CGGCCCTTGCTCGGCACTCCGTGGTGGTGTCTGCTCCCTTCTCCCTGCAATGCTGTGGGTCTGC	2972
Db	2882	CGGCCCTTGCTCGGCACTCCGTGGTGGTGTCTGCTCCCTTCTCCCTGCAATGCTGTGGGTCTGC	2941
QY	2973	TCTGAGTGTGAAGAGTTCGGTGGGTTAACTGTGTGCTTACTGAACCTGGCAATTAACATTC	3032
Db	2942	TCTGAGTGTGAAGAGTTCGGTGGGTTAACTGTGTGCTTACTGAACCTGGCAATTAACATTC	3001
QY	3033	ACCCCTGCAAGCCAAA 3048	
Db	3002	ACCCCTGCAAGCCAAA 3017	

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RESULT 4
US-10-037-270-20
/ Sequence 20, Application US/10037270
/ Publication No. US20030104529A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunging
/ APPLICANT: Wang, Duntui
/ APPLICANT: Wang, Zhimei
/ APPLICANT: Tillinghast, John
/ APPLICANT: Dimahe, Radoje T.
/ TITLE OF INVENTION: No. US20030104529A1 Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides

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FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: Pf_Fl_genes Version 1.0
SEQ ID NO 20
LENGTH: 2840
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (206)..(1711)
US-10-037-270-20

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Query Match      89.3%; Score 2791.2; DB 15; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 50 TGCTGAGGTTCTGCTAGCCGAGAGCGCTGATCTGCGCGCGCTGCTGCGCGCTGCTG
DB 45 TGCTGAGGTTCTGCTAGCCGAGAGCGCTGATCTGCGCGCGCTGCTGCGCGCTGCTG
QY 110 GAGCGGATTCTGCGCGCGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG
DB 105 GAGCGGATTCTGCGCGCGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCG
QY 170 CTTCCCTGTCAGCAACGCGCGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG
DB 165 CTTCCCTGTCAGCAACGCGCGCTGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG
QY 230 CTCTGCGCGCAAGAGAACTTAACCAAGCCATCGAGAGTGACTGACAGATGATTTG
DB 225 CTCTGCGCGCAAGAGAACTTAACCAAGCCATCGAGAGTGACTGACAGATGATTTG
QY 290 GACAGTCATCAAGACTGAGAGGTTTGTGAATCTTCCGCGCAAGAGCAAGACAG
DB 285 GACAGTCATCAAGACTGAGAGGTTTGTGAATCTTCCGCGCAAGAGCAAGACAG
QY 350 GCAGCTGCAACCTGCAAGAACTTCCAGAAAGCGCGAGCGCGCAAGAGTGGGAAAGCTG
DB 345 GCAGCTGCAACCTGCAAGAACTTCCAGAAAGCGCGAGCGCGCAAGAGTGGGAAAGCTG
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DB 405 CCAAGAGAGATAGGCACTCTCAAGATGAGAGCAATCCCAATCTCAAGTGTG
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QY 710 TCCATCTGCTAAGCTAGAAAATGCTCATCAAGAGCGCTGTGAGACCCCGCAGTATC
DB 705 TCCATCTGCTAAGCTAGAAAATGCTCATCAAGAGCGCTGTGAGACCCCGCAGTATC
QY 770 TGGCCCAAGAGTGTAGCGCGGCAAGCGGATGAGACGCTCTGTGAGCTGTGGGCAATTG
DB 765 TGGCCCAAGAGTGTAGCGCGGCAAGCGGATGAGACGCTCTGTGAGCTGTGGGCAATTG

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QY 890 ATGATTATGAGAACCATGATTAAGAACTCTTCCGCAAAATCTTGCTGTGATATGAGT
DB 885 ATGATTATGAGAACCATGATTAAGAACTCTTCCGCAAAATCTTGCTGTGATATGAGT
QY 950 TTGACCTTCATATTTGGGATGATTTTTCAGGAGGCAAGCAAGCAAGCTGTCAAGAGCTGA
DB 945 TTGACCTTCATATTTGGGATGATTTTTCAGGAGGCAAGCAAGCAAGCTGTCAAGAGCTGA
QY 1010 TGGAGGTGAGCAAGCAAGCGGATCACTGCAAGAGAGGCAATCTCCATGATGATTT
DB 1005 TGGAGGTGAGCAAGCAAGCGGATCACTGCAAGAGAGGCAATCTCCATGATGATTT
QY 1070 CTGGCAATGCTGCTTCTGATTAAGAACTATGATGATGCTGTGCTGCTGCAAGTGAAGA
DB 1065 CTGGCAATGCTGCTTCTGATTAAGAACTATGATGATGCTGTGCTGCTGCAAGTGAAGA
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DB 1125 ACTTTGCGAGGCGCAAGTGAAGAGGCTGTCCAGTGAACCAACCTCATGAAGCGCTCC
QY 1190 GGGCAACAGAGAGTCCAGCAAGCGCTGAGCCAGTGGGCTCAAGCAAGCACTGCA
DB 1185 GGGCAACAGAGAGTCCAGCAAGCGCTGAGCCAGTGGGCTCAAGCAAGCACTGCA
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DB 1245 CCCCAGGCGCTGCAAGTGGGCGCAAGCTGCACTGCAAGTGAAGCTTACTGAGCCCTG
QY 1310 AGGTGATGCTGCTGCTGCTGCAAGAGTATGATGATGATGATGATGATGATGATGATG
DB 1305 AGGTGATGCTGCTGCTGCTGCAAGAGTATGATGATGATGATGATGATGATGATGATG
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DB 1425 ATGGAAGCTCACTCAAGCACTGATGGAAGTGTCAACCCAGTCACTGACAGAGAGCTTA
QY 1490 CTCACGCCATGATGGAAGAGCCACACAGCCACAGAAAGAGCACTGTGCCACACCC
DB 1485 CTCACGCCATGATGGAAGAGCCACACAGCCACAGAAAGAGCACTGTGCCACACCC
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DB 1605 CGGACAGCAACACCCCAAGAGGCGGCGCAAGGCGCAAGCTTCAACCTCTGTAAGGAGAG
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DB 1725 TGAAGGAGGAGCAAGGAGTGGGAGAGAGGCTGGAAGAGTGAAGAGAGGCTTCTCACTGTA
QY 1790 CATAGAGTCACTGAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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QY 1850 ACTAGAGGAGTCAAGGAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
DB 1845 ACTAGAGGAGTCAAGGAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

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QY 1910 GCCAGTGGAGGGGCGGGCCGACGCCCTGATGATTCCTTGTGCTTTCTGCTTTTG 1969
Db 1905 GCCAGTGGAGGGGCGGGCCGACGCCCTGATGATTCCTTGTGCTTTCTGCTTTTG 1964
QY 1970 CTAGCTTACCGATTCTGCTTGTGGGATGCTGCTTAAAGGATCTCAGGGGCTCC 2029
Db 1965 CTAGCTTACCGATTCTGCTTGTGGGATGCTGCTTAAAGGATCTCAGGGGCTCC 2024
QY 2030 TGTCTCCTTCCCTTCCCTTCTGCTGCTCAATTCCTTAAAGGAGGCTGAGGCTCC 2089
Db 2025 TGTCTCCTTCCCTTCCCTTCTGCTGCTCAATTCCTTAAAGGAGGCTGAGGCTCC 2084
QY 2090 ACACTCTCCAGGCGCTTAACTTGGGCGGCTTGCCTTGAAGAGCTGCTCCAGCGAG 2149
Db 2085 ACACTCTCCAGGCGCTTAACTTGGGCGGCTTGCCTTGAAGAGCTGCTCCAGCGAG 2144
QY 2150 CCCTGTGAGGGGTCTTAAAGCTCTGCAATGAAGTGTGTGCTGTGTGGGCTGC 2209
Db 2145 CCCTGTGAGGGGTCTTAAAGCTCTGCAATGAAGTGTGTGCTGTGTGGGCTGC 2204
QY 2210 TCTAGAGCGATACAGGCTGTGTATAGAGATGCAAAAGATAGGGCAATATGTTAAT 2269
Db 2205 TCTAGAGCGATACAGGCTGTGTATAGAGATGCAAAAGATAGGGCAATATGTTAAT 2264
QY 2270 CCAGACTTGGCATGAGCTGAGATCTGCTCACTAGCTGTGAGGCTCCTCAGAGTGA 2329
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QY 2330 GAGAAATAGTAGAGGAGGAGAGAGCTTCAATTTTGTCTTCTTCTTCTTCTTCTT 2389
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QY 2390 GTTATTTCTGCTTTTCCGAGTCTGCAAGTGGCTGCTTAACTTCAATGAGC 2449
Db 2385 GTTATTTCTGCTTTTCCGAGTCTGCAAGTGGCTGCTTAACTTCAATGAGC 2444
QY 2450 CTCTAAGGAGAAAGAGAGAAATTAAGACGTGCGAATAGAGACCTGCGAGGGCAGATGA 2509
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QY 2510 AGCCGAGCAACCAAGTGTCCGAGCTTACTGAGTCTTAACTTCTGAGGCGAAAGAGGAGC 2569
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QY 2630 CCACCTTAAAGGGGCTTCTGCAATGAGCAATACATCATATGATTTGAGAGTTTGGCCTT 2689
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QY 2690 TACAGGGGGAGATTTTCTGCTGATGCAATGAAATGAAAGAGAACTCCCTTCTTCTA 2749
Db 2685 TACAGGGGGAGATTTTCTGCTGATGCAATGAAATGAAAGAGAACTCCCTTCTTCTA 2744
QY 2750 CAGCTCACTTCTATCAGAGGCGCGAGTGTCTCAGAGCCATGATGATTTTCTTCTGAG 2809
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Db 2805 ATGAGAGATAGGGTTAACTCCCGAGTTTCTGAG 2840

RESULT 5
US-10-117-722-20
; Sequence 20, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie
; APPLICANT: Dimanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B2IP
; CURRENT APPLICATION NUMBER: US/10/117,722
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: PL_Fl_genes Version 1.0
; SEQ ID NO 20
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)..(1711)
US-10-117-722-20

Query Match 89.3%; Score 2791.2; DB 16; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 TGTGAGAGTTGCTAGCCGAGAGGCTGCAATCTGAGGCGCGCTTCCCGGCTGCTG 109
Db 45 TGTGAGAGTTGCTAGCCGAGAGGCTGCAATCTGAGGCGCGCTTCCCGGCTGCTG 104
QY 110 GAGGAGATTTCTGCGCGCGCTTCCCGGAGCCCTGCGGCGCGCGCTGAGCGGATCACT 169
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Db 165 CTTCCCTGTGCAACCGGCGCTGAGGTTAGAGCTGCGAATGCGCTTTGGTGTGTA 224
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Db 225 CTCTGAGGAGAGAGAGAGATTAACAGCCATGAGGAGTGAATGATGATTTGG 284
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QY 410 CCAAGAGAGATAGGATCTCTCAAGATGTAAGATCCCAATCTCAAGCTGCTG 469
Db 405 CCAAGAGAGATAGGATCTCTCAAGATGTAAGATCCCAATCTCAAGCTGCTG 464
QY 470 ATGTGTTGTGACCGGCAAGAGATTTATCTTCTCTGAGCTGCGCAAGGAGAGAG 529
Db 465 ATGTGTTGTGACCGGCAAGAGATTTATCTTCTCTGAGCTGCGCAAGGAGAGAG 524
QY 530 TGTTTGATCTGATCTCTGACCAAGGCTTCTCTGAGCGAGCAAGAGCAAGCTGCTG 589
Db 525 TGTTTGATCTGATCTCTGACCAAGGCTTCTCTGAGCGAGCAAGAGCAAGCTGCTG 584
QY 590 GGCAGTCTGAGGCGCTGAGCTTCTGCACTCACTCAATGATGTCAGAGATCTCA 649
Db 585 GGCAGTCTGAGGCGCTGAGCTTCTGCACTCACTCAATGATGTCAGAGATCTCA 644
QY 650 AGCTGAGAGACTGTGTTACTTCAACCGGCTGAGAGACTGCAAGATTTCTCATCTGACT 709
Db 645 AGCTGAGAGACTGTGTTACTTCAACCGGCTGAGAGACTGCAAGATTTCTCATCTGACT 704
QY 710 TCCATCTGCTAAGCTAAGAAATGCGCTCATCAAGAGACCTGTGTGGAGCCCCGAGTATC 769

Thu Apr 29 08:44:17 2004

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Page 9

Db	705	TCATCTGCTTAAGCTAAGAAATAGCCTCATCAAGAGCCCTGTGGAGACCCCGAGATATC	764
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Db	765	TGGCCCCAGAGGTGTAGCCGCGACGGATAGGACGCCCTGTGACTGCTGTGGCCATTG	824
Qy	830	GAGTCATCATGTACATCTGCTTTACGGCAATCCACTTTCTATGAGAGGTGAAAGAG	889
Db	825	GAGTCATCATGTACATCTGCTTTACGGCAATCCACTTTCTATGAGAGGTGAAAGAG	884
Qy	890	ATGATTATGAGAACCATGATTAAGATTCTTTCCGCAAGATCTCGCTGTGACTTATGAGT	949
Db	885	ATGATTATGAGAACCATGATTAAGATTCTTTCCGCAAGATCTCGCTGTGACTTATGAGT	944
Qy	950	TTGACTCTCCATATTTGGGATGATTTTCCGAGGAGCAAGAAGCTGGTCAAGAGGTGA	1009
Db	945	TTGACTCTCCATATTTGGGATGATTTTCCGAGGAGCAAGAAGCTGGTCAAGAGGTGA	1004
Qy	1010	TGGAGGTGAGCAAGACCAAGCGGATCTCATGAGAGAGCCATCTCCATGAGTGAATTT	1069
Db	1005	TGGAGGTGAGCAAGACCAAGCGGATCTCATGAGAGAGCCATCTCCATGAGTGAATTT	1064
Qy	1070	CTGGCAATGCTGCTTCTGATTAAGAACTCAAGGATGTTGTGTGCTGCCAGATTGAAAGA	1129
Db	1065	CTGGCAATGCTGCTTCTGATTAAGAACTCAAGGATGTTGTGTGCTGCCAGATTGAAAGA	1124
Qy	1130	ACTTTGCGAGGGCCAAATGGAAGAGGCTGTCGAGTGAACCAACCTCATGAAACGCGTCC	1189
Db	1125	ACTTTGCGAGGGCCAAATGGAAGAGGCTGTCGAGTGAACCAACCTCATGAAACGCGTCC	1184
Qy	1190	GGGACACAGAGACAGTCCAGACCGGCTCAGCCCACTGAGCTCAGCCACAGACTGSCCA	1249
Db	1185	GGGACACAGAGACAGTCCAGACCGGCTCAGCCCACTGAGCTCAGCCACAGACTGSCCA	1244
Qy	1250	CCCCGGGGGCTGACAGTGGGGCCACAGCTGACGTGCGAGTGAAGCTTACCTCAGCCCTG	1309
Db	1245	CCCCGGGGGCTGACAGTGGGGCCACAGCTGACGTGCGAGTGAAGCTTACCTCAGCCCTG	1304
Qy	1310	AGGATGATGCTGCTCGTGTCTGCAAAAGATGATTAATGTGGCCCCCGGACACCTGATGSCCA	1369
Db	1305	AGGATGATGCTGCTCGTGTCTGCAAAAGATGATTAATGTGGCCCCCGGACACCTGATGSCCA	1364
Qy	1370	CCCCAGCCACAGATGAGTAGTGGCCACCCACGACATGATGAGAGGTGACCCCGAGCCACCG	1429
Db	1365	CCCCAGCCACAGATGAGTAGTGGCCACCCACGACATGATGAGAGGTGACCCCGAGCCACCG	1424
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Db	1425	ATGGAACATCACTCCAGCCACTGATATGAGGAGTGTCACTCCAGTCACTGACAGGACGCTA	1484
Qy	1490	CTTCAGCCACTGATGAGAGAGCCACACAGCCACAGAAAGAGACCTGTGCCACCAACC	1549
Db	1485	CTTCAGCCACTGATGAGAGAGCCACACAGCCACAGAAAGAGACCTGTGCCACCAACC	1544
Qy	1550	AAAGCAATGCCATGCTGTGGCCCAAGGACAGTGTGCCACCCCTGAGCCGGGCTATGGCCAGC	1609
Db	1545	AAAGCAATGCCATGCTGTGGCCCAAGGACAGTGTGCCACCCCTGAGCCGGGCTATGGCCAGC	1604
Qy	1610	CGGACAGACAGCCCCAGAGGGCCGACAGGCCAGGCTCCACCTCTAATGTAAGAGGGAAG	1669
Db	1605	CGGACAGACAGCCCCAGAGGGCCGACAGGCCAGGCTCCACCTCTAATGTAAGAGGGAAG	1664
Qy	1670	AGGCTGTGCTTATGCCAGGAGTCTCAAGAGGAGAGCCAGCTGATGAGCAGCCTGG	1729
Db	1665	AGGCTGTGCTTATGCCAGGAGTCTCAAGAGGAGAGCCAGCTGATGAGCAGCCTGG	1724
Qy	1730	TGAGGGGGGGATGGGGATGGGCAAGAGGGGTGGAGATGATGAGGGGCTTCTCACTGTGA	1789
Db	1725	TGAGGGGGGGATGGGGATGGGCAAGAGGGGTGGAGATGATGAGGGGCTTCTCACTGTGA	1784
Qy	1790	CATGAGATCACTGGACATGATGCTCGTCCCTCCCATGGCCCCCATCCAGATGGGGGATGA	1849

D	1785	CATGAGTCACTGGCATGATGECCTCGCTCCCAACGACCCCAATCCAGATGGGGATA	1844
Q	1850	ACTAGGGGTACGGGAGAGCAGTCTCGTCTCTGTGTATGTGTGAATGTGGGAG	1909
D	1845	ACTAGGGGTACCGGGAGAGCAGTCTCGTCTCTGTGTATGTGTGAATGTGGGAG	1904
Q	1910	GCCAGTGGCAGGGCCGGCCCAAGCCCTTGATGATATCTTGTGGCTTTCTGTCTTGG	1969
D	1905	GCCAGTGGCAGGGCCGGCCCAAGCCCTTGATGATATCTTGTGGCTTTCTGTCTTGG	1964
Q	1970	CTAGCTTCACACAGTTTCTGTTCCTGTGGGATGCTGTCTAGAGGATATCTAGGGGAGCTCC	2029
D	1965	CTAGCTTCACACAGTTTCTGTTCCTGTGGGATGCTGTCTAGAGGATATCTAGGGGAGCTCC	2024
Q	2030	TGCTCTCTTCCCTTCCCTCTTGTGCTCAATTCCTCTAGGACGGCCCTGACAGTCCC	2089
D	2025	TGCTCTCTTCCCTTCCCTCTTGTGCTCAATTCCTCTAGGACGGCCCTGACAGTCCC	2084
Q	2090	ACACTCTCCAGGCGCTTAACTTTGGGCGGCTTGGCCCTGAGAGTGTCTTCAAGCAGG	2149
D	2085	ACACTCTCCAGGCGCTTAACTTTGGGCGGCTTGGCCCTGAGAGTGTCTTCAAGCAGG	2144
Q	2150	CCCTGTAGAGGCTTTTAGTCTCTGACACATGAAGAGTGTGCGCTGTGTGTGGGCTGC	2209
D	2145	CCCTGTAGAGGCTTTTAGTCTCTGACACATGAAGAGTGTGCGCTGTGTGTGGGCTGC	2204
Q	2210	TCTAGAGCAGATPACAGGCTGTGTATAGAGATCAGAAAGGTAGGGCAGATGTTTAACT	2269
D	2205	TCTAGAGCAGATPACAGGCTGTGTATAGAGATCAGAAAGGTAGGGCAGATGTTTAACT	2264
Q	2270	CCAGACTTGGCACAATGGCTTAGGATPCTGCTCACTAGCTGTGAGGTCTCAGAGATGA	2329
D	2265	CCAGACTTGGCACAATGGCTTAGGATPCTGCTCACTAGCTGTGAGGTCTCAGAGATGA	2324
Q	2330	GAGAAATGATGAGAGGGGCAAGATTTTCTTCTTCTTAAGACCTGTATTTGT	2389
D	2325	GAGAAATGATGAGAGGGGCAAGATTTTCTTCTTCTTAAGACCTGTATTTGT	2384
Q	2390	GTTATTTCCGCGCTTTCGAGTCCCTGAGTGGGCTGCGCTGATCCCTGAACCTCATGAGC	2449
D	2385	GTTATTTCCGCGCTTTCGAGTCCCTGAGTGGGCTGCGCTGATCCCTGAACCTCATGAGC	2444
Q	2450	CTCTAAGGAAAGAGGAGAACATTTAGACCTGGCAATGAGACCTGGCAGGGCAGATACA	2509
D	2445	CTCTAAGGAAAGAGGAGAACATTTAGACCTGGCAATGAGACCTGGCAGGGCAGATACA	2504
Q	2510	AGCCAGACACCAGATGTCCAGGCTTACTGGGCTTACCTGTGGCCAAACAGGAGAGGC	2569
D	2505	AGCCAGACACCAGATGTCCAGGCTTACTGGGCTTACCTGTGGCCAAACAGGAGAGGC	2564
Q	2570	TGATATCTCTGTGTCTTCTTAATGCGCACCTTCCTAATTCACGCCCAAGTCCCT	2629
D	2565	TGATATCTCTGTGTCTTCTTAATGCGCACCTTCCTAATTCACGCCCAAGTCCCT	2624
Q	2630	CCACCCCTAAGGGGGTTTCTGTGATGGCAATACATCAATCTGAATTTGAGATTTGCCCTT	2689
D	2625	CCACCCCTAAGGGGGTTTCTGTGATGGCAATACATCAATCTGAATTTGAGATTTGCCCTT	2684
Q	2690	TACAGGGGAGATTTTCTGTCTCACTTCAACATGAATGAAGAGAACTCCCTCTTTCTA	2749
D	2685	TACAGGGGAGATTTTCTGTCTCACTTCAACATGAATGAAGAGAACTCCCTCTTTCTA	2744
Q	2750	CAGCTCACTTCTATCAAGGCCACAGGTGCTCAGAGCCACATTTAGTGTCTTTTCTGGG	2809
D	2745	CAGCTCACTTCTATCAAGGCCACAGGTGCTCAGAGCCACATTTAGTGTCTTTTCTGGG	2804
Q	2810	ATGAGGAATGAGGTTAACTCCCACTTTCTGGAG	2845
D	2805	ATGAGGAATGAGGTTAACTCCCACTTTCTGGAG	2840

RESULT 6
INS 10 425 114-26867

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/ Sequence 26867, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ. ID NOS: 75128
/ SEQ. ID NO 26867
/ LENGTH: 2895
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB4654-060-B3_FLI
US-10-425-114-26867

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Query Match      89.0%; Score 2780.8; DB 13; Length 2895;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2885; Conservative 0; Mismatches 2; Indels 93; Gaps 1;

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QY 126 CCGTCCCGGAGCGCTCGGCGCGCGTCTGGAGCGGATTTGCGCG 185
DB 61 CCGTCCCGGAGCGCTCGGCGCGCGTCTGGAGCGGATTTGCGCG 120
QY 186 CCGCGCTGCAGTTAGAGCTGGCAATGCCGTTGGGTGTGACCTCGGCGCAAGAA 245
DB 121 CCGCGCTGCAGTTAGAGCTGGCAATGCCGTTGGGTGTGACCTCGGCGCAAGAA 180
QY 246 GAATTAACCAAGCATCGAGGTGACTGACAGATATGATTTGGGACAGGTCACTAAGAC 305
DB 181 GAATTAACCAAGCATCGAGGTGACTGACAGATATGATTTGGGACAGGTCACTAAGAC 240
QY 306 TGAAGAGTTTGTGAATCTTCCGGGCAAGCAAGACGACGAGGACCTGACACCTG 365
DB 241 TGAAGAGTTTGTGAATCTTCCGGGCAAGCAAGACGACGAGGACCTGACACCTG 300
QY 366 CAAGAAATTCAGAGGCGGACCGCGCAAGGTGCGGAAAGCTGCCAAGACGAGTAGG 425
DB 301 CAAGAAATTCAGAGGCGGACCGCGCAAGGTGCGGAAAGCTGCCAAGACGAGTAGG 360
QY 426 CATCTCAAGATGATGAGATCCCAATCTTACAGCTGTGTGATGTGTTGTGACCGG 485
DB 361 CATCTCAAGATGATGAGATCCCAATCTTACAGCTGTGTGATGTGTTGTGACCGG 420
QY 486 CAAGAGTACTTATCTTCTGTGAGCTGCGCAAGGAGGAGGATTTGACTGATCTT 545
DB 421 CAAGAGTACTTATCTTCTGTGAGCTGCGCAAGGAGGAGGATTTGACTGATCTT 480
QY 546 GAGACGAGGCTACTACTCGGAGGAGACACAGAACAGTGTGTCGGCAAGCTCTGAGGC 605
DB 481 GAGACGAGGCTACTACTCGGAGGAGACACAGAACAGTGTGTCGGCAAGCTCTGAGGC 540
QY 606 CGAGGCTTATTTGCACTCACTCAAGATCTGCAAGAAATCTCAAGTGGAGAACTGGT 665
DB 541 CGAGGCTTATTTGCACTCACTCAAGATCTGCAAGAAATCTCAAGTGGAGAACTGGT 600
QY 666 TTAATCAACCGGCTGAAGAACTGAAGATTGTATCATGATGATTCATCTGCTAAGCT 725
DB 601 TTAATCAACCGGCTGAAGAACTGAAGATTGTATCATGATGATTCATCTGCTAAGCT 660
QY 726 AGAAATGCGCTCATCAAGAGCGCTGTGGAGCCCCGAGTATCTGCGCCCAAGGTGT 785

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DB 661 AGAAATGCGCTCATCAAGAGCGCTGTGGAGCCCCGAGTATCTGCGCCCAAGGTGT 720
QY 786 AGCGCGGAGGATGATGAGAGCGCTGTGAGCTGTGGGCAATGAGTCACTATGATCAT 845
DB 721 AGCGCGGAGGATGATGAGAGCGCTGTGAGCTGTGGGCAATGAGTCACTATGATCAT 780
QY 846 CCGCTTTTCAAGGCAATCCACTTTCTATGAGAGGTGAGAAAGATGATTTATGAGAACCA 905
DB 781 CCGCTTTTCAAGGCAATCCACTTTCTATGAGAGGTGAGAAAGATGATTTATGAGAACCA 840
QY 906 TGAATGAATCTCTTCCGCAAGATCTGCTGTGATGATGATGATGATGATGATGATG 965
DB 841 TGAATGAATCTCTTCCGCAAGATCTGCTGTGATGATGATGATGATGATGATGATG 900
QY 966 GATGATATTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1025
DB 901 GATGATATTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 1026 CCAGCGGATCACTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1085
DB 961 CCAGCGGATCACTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1086 TGAATGAATCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1145
DB 1021 TGAATGAATCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1146 GTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205
DB 1081 GTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1206 CAGACGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1265
DB 1141 CAGACGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1195
QY 1266 TGGGAGCAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1325
DB 1196 TGGGAGCAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1195
QY 1326 TGCTGCAAGAGATGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1385
DB 1196 TGCTGCAAGAGATGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1227
QY 1386 AAGTGCACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1445
DB 1228 AAGTGCACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1287
QY 1446 AGCAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1505
DB 1288 AGCAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1347
QY 1506 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1565
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QY 1626 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1685
DB 1468 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1527
QY 1686 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1745
DB 1528 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1587
QY 1746 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1805
DB 1588 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1647
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[illegible]

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Db	2848	GCCCTACTGAACCTGGCAATTAACATACACCTGAAAGCC	2887
Db	2788	CTTCTCCCTGCAAGCCGCTGGGCTGCTCGATGATGAAAGGCGGGTTAACTGT	2847
QY	2946	CTTCTCCCTGCAAGCCGCTGGGCTGCTCGATGATGAAAGGCGGGTTAACTGT	3005

RESULT 7
US-10-425-114-26845

Sequence 26849, Application US/10425114

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/425,114

NUMBER OF SEQ ID NOS. 73128

SEQ ID NO 26849

LENGTH: 2000
TYPE: DNA

ORGANISM: *Homo sapiens*

OTHER INFORMATION: CLONE ID: LIB4654-022-E3_FLI

US-10T-01-20

Query Match	Score	DB	Length
88.8%;	2773.8;	13;	2880;

Matches 2678; Conservative 0; Mismatches 2; Indels 93; Gaps 1;

67 CCGAAGCGGCTGCATCTGCGCGCCGCGTCTGACCCCGCGTTCCTCGGAGCGGATTCTGCCCCGC 126

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127 CGTCCCTGAGCCCTTCGGCCCTCCGCTGAGCCCTGGATCACTTCCCTCCCTGTGACCAACC 186

Db 61 CGTCCCCGAGCCCTCGCGCCCCCGCTGAGCCCCGGATCACTTCTCTCCCTGTGACCAACC 120

187 GGGGCTGACGTTAGAGCCTGCAATGCCGTTGGTGCTGACTCTGGCGACAAGAAG 246

121 AGGCTGCAAGCTTACGACATGCGCTTTCCTCTCTGACTCTGCGCGGCAAGAGAC 180

23 / AACCAATACACACATCGAAGAGACAGACAGAAAGAAAGAGACAGAGCAACAGAGC 308

Db 181 AACTATAACCGCCATCGGAGGTGACTGACAGATATGATTTGGGACAGGTCAAGACT 240

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241 GAGGACTTTTGTGAATCTTCCGGCCCAAGACAAGCCTGCACCTGC 300

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DB 301 AAGAGTTCAGAGCGGACCGCAAGTGGGAAAGCTGCCAAGACGAGATAGGC 360

427 ATCCTCAGATGGTGAAGCATCCCAACATCCTACAGCTGGTGATGTTGTGACCCG 486

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487 AAGGAGTACTTTATCTTCCTGGAGCTGGCCACCGGAGAGGAGGTGTTTGAACTGGATTCTTG 546

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547 GACCAGGGCTACTACTCGAGCGAGACACAAGCAACGTGTGTAACGGCAAGTCTCGAGGCC 606

Db 481 GACCAGGGCTACTCGAGCGAGACACAAGCAACGTGTACGGCAAGTCTTGAGGCC 540

QY 607 GTGGCTATTGTGCACTCACTCAAGATGTCGACAGAAATCTCAAGCTGGAGAACTTGTT 666
Db 541 GTGGCCATTATTGACTCACTCAAGATGTCGACAGGAATCTCAAGCTGGAGAACTTGTT 600
QY 667 TACTACACCGGGCTGAAGAACTGGAAGATTGTCAATGATGATCTTGCATCTGGTATAGCTA 726
Db 601 TACTACACCGGGCTGAAGAACTGGAAGATTGTCAATGATGATCTTGCATCTGGTATAGCTA 660
QY 727 GAAATATGCTCTCAAGAGAGCCCTGTGGACCCCGAGATCTGGCCCGAGAGTGGTA 786
Db 661 GAAATATGCTCTCAAGAGAGCCCTGTGGACCCCGAGATCTTGGCCCGAGAGTGGTA 720
QY 787 GAGCGGACGAGGATGAGACCCCTGTGGACTGTGGGCCATTGAGATCAATGATGATC 846
Db 721 GAGCGGACGAGGATGAGACCCCTGTGGACTGTGGGCCATTGAGATCAATGATGATC 780
QY 847 CTGCTTTCAGGCAATCCACTTTCATGAGAGAGTGGAGAGATGATTATGAGAACAT 906
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Db 841 GATAGAAATCTCTCCGCAAGATCTTGCGCTGTGATCAATGATGATGATCTCCATATGG 900
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Db 901 GATGATATTCGAGAGGACGCAAGACCTGTGTCAAGAGCTGATGAGAGTGGAGCAAGAC 960
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QY 1267 GGGGACCAAGCTGACGCTGAGTGAAGTAACTCAAGCCCTGAGGGGTGATGCTGCTGT 1326
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Db 1195 -----GAGACCCCTAGTGGCCACCCCGAGCCACAGATGGA 1227
QY 1387 AGTGGCAAGCCCAAGCACTGATGAGAGTGTCAACCCCAAGCCACCGATGAGAGATCACTTCA 1446
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Db 1648 GATGCTCTGCTCCGCCATGCCCCACATCCCAAGTGGGAGATTAAGAGGGGTCAAGGAG 1707
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Db 1708 AGCAGTCTGTCTCTGTGTATGT 1767
QY 1927 CCCCCCCCCCTGACATGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1986
Db 1768 CCCCCCCCCCTGACATGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1827
QY 1987 TGTTCCTGTGAGATGCTGTCTGAGGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2046
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QY 2167 GAGTCTGCAATAGAGT 2226
Db 2008 GAGTCTGCAATAGAGT 2067
QY 2227 GCTGTATAGAGATGACGAGAAAGGTAGAGGAGTGTATGTTAAATGTCACACTTGGCACATGG 2286
Db 2068 GCTGTATAGAGATGACGAGAAAGGTAGAGGAGTGTATGTTAAATGTCACACTTGGCACATGG 2127
QY 2287 CTAGGATACTGCTCACTAGCTGTGAGGTCTTCAGAGTGGAGAGATGATGAGAGG 2346
Db 2128 CTAGGATACTGCTCACTAGCTGTGAGGTCTTCAGAGTGGAGAGATGATGAGAGG 2187
QY 2347 CAGAACTTCAATTTTGTCTTCTTAAAGACCTGTATTTGTGTATTTTCTGCTTTC 2406
Db 2188 CAGAACTTCAATTTTGTCTTCTTAAAGACCTGTATTTGTGTATTTTCTGCTTTC 2247
QY 2467 CGAGTCTGAGTGGGCTGCGCTGTACCTGAACTGATGAGCTTAAGAGAAAGAGG 2466
Db 2248 CGAGTCTGAGTGGGCTGCGCTGTACCTGAACTGATGAGCTTAAGAGAAAGAGG 2307
QY 2467 AACATTTAGACGTGGCAATGAGACTGGAGGAGAGTGAAGAGGAGAGGAGGAGGAGGAGGAG 2526
Db 2308 AACATTTAGACGTGGCAATGAGACTGGAGGAGAGTGAAGAGGAGAGGAGGAGGAGGAGGAG 2367
QY 2527 CCGAGCTTACTGAGTCTTACCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2586
Db 2368 CCGAGCTTACTGAGTCTTACCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2427
QY 2587 TCTTGAAGAGCCACTCTCAATCAATCTGAGCCCAAAATCTCTTCCACACCTTGAAGGGGCTTG 2646
Db 2428 TCTTGAAGAGCCACTCTCAATCAATCTGAGCCCAAAATCTCTTCCACACCTTGAAGGGGCTTG 2487
QY 2647 CTGATGGCAATTAATCAATTAATGATTTGAGAGGTTGAGGAGGAGGAGGAGGAGGAGGAGGAG 2706
Db 2488 CTGATGGCAATTAATCAATTAATGATTTGAGAGGTTGAGGAGGAGGAGGAGGAGGAGGAGGAG 2547
QY 2707 TGTCTAGTTCAACATGAATGAAGAGAACTCCCTCTTTCTACAGCTCACTTATCAG 2766
Db 2548 TGTCTAGTTCAACATGAATGAAGAGAACTCCCTCTTTCTACAGCTCACTTATCAG 2607
QY 2767 AGGCCAGAGTCTCAAGAGCCACTTAAGTTGCTTTTCTGTGGATGAGGAAGTGAAGGTTA 2826

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Q _Y	AACTCCCAAGTTTCCGAGGAGGCT	CTGACAGGTGCCCTTATCAGACCCACACAG	2886						
D _b	AACTCCCAAGTTTCCGAGGAGGCT	CTGACAGGTGCCCTTTGTCAACCCACACAG	2727						
Q _Y	CTCGAATAGGACCAATTGGT	CCTCGCCCTGCTCGGCACTCCGTGGTGTCTGCCC	2946						
D _b	CTCGAATAGGACCAATTGGT	CCTCGCCCTGCTCGGCACTCCGTGGTGTCTGCCC	2787						
Q _Y	TTCCTCCTGCATCCGTGGGT	CTGCTCGAGTGTGAAGATCGATGGGTTAACTGTG	3006						
D _b	TTCCTCCTGCATCCGTGGGT	CTGCTCGAGTGTGAAGATCGATGGGTTAACTGTG	2847						
Q _Y	CCCTACGAACCTGGCAATTAACAT	CACCTTGC	3039						
D _b	CCCTACGAACCTGGCAATTAACAT	CCTCCCTGC	2880						

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RESULT 8
US-10-425-114-26958
; Sequence 26958: Application US/10425114
; Publication NO: US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 73128
; SEQ ID NO 26958
; LENGTH: 3236
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: Clone ID: LIB4676-058-A2_FLI
; US-10-425-114-26958

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Query Match	86.7%	Score 2709.2;	DB 13;	Length 3236;
Best Local Similarity	92.2%;	Pred. No. 0;		
Matches 2982;	Conservative	0;	Mismatches 3;	Indels 251; Gaps 2;

QY	61	CGCTAGCCGAAAGCGGCTGCACTCGGCGGCCGCGCTCCGCCGCGTGTCTCGAGCGCAATTC	120
Db	1	CGCTAGCCGAAAGCGGCTGCACTCGGCGGCCGCGCTCCGCCGCGTGTCTCGAGCGCAATTC	60
QY	121	GCCCGCGCTCCCGGAGCCCTCGGCGGCCCGCGTAGACCCGGATACATTCCTCCCTGTGA	180
Db	61	GCCCGCGCTCCCGGAGCCCTCGGCGGCCCGCGTAGACCCGGATACATTCCTCCCTGTGA	120
QY	181	CCAACCGCGCCTCAGATTAGACCTGGACCTGGCAATGCCGTTGGGTGTGTACTCTGGGCGAC	240
Db	121	CCAACCGCGCCTCAGATTAGACCTGGACCTGGCAATGCCGTTGGGTGTGTACTCTGGGCGAC	180
QY	241	AAGAAGAACTATAACAGCCATCGGAGGTCGATCAATATGATTGGGACAGGTATC	300
Db	181	AAGAAGAACTATAACAGCCATCGGAGGTCGATCAATATGATTGGGACAGGTATC	240
QY	301	AAGCTAGGAGATTTGTGAAATCTTCGCGGCGCAAGACAAGACGACAGCGAACTGCAC	360
Db	241	AAGCTAGGAGATTTGTGAAATCTTCGCGGCGCAAGACAAGACGACAGCGAACTGCAC	300
QY	361	ACCTGCAAGAACTCCAGAAAGCGGGACGGCCGCAAGAGTTCGGAAAGCTGCCAATAAGAG	420
Db	301	ACCTGCAAGAACTCCAGAAAGCGGGACGGCCGCAAGAGTTCGGAAAGCTGCCAATAAGAG	360

QY	421	ATAGGCAATCTCAAGATAGGGAAGCATGCCAAATCCATCAAGCTGGGATGTGTGTG	480
Db	361	ATAGGCAATCTCAAGATAGTGAAGCATCCCAATCTCAAGCTGGGATGTGTGTG	420
QY	481	ACCGGCAAGGATGATCTTATCTTCTGGAGCTGGCCAAGGGAGGAGGTGTGACTGG	540
Db	421	ACCGGCAAGGATGATCTTATCTTCTGGAGCTGGCCAAGGGAGGAGGTGTGACTGG	480
QY	541	ATCTGGAACCAAGGCTTACTCTGGAGCCGACACAAAGCAAGCTGGTACGGCAATCTCTG	600
Db	481	ATCTGGAACCAAGGCTTACTCTGGAGCCGACACAAAGCAAGCTGGTACGGCAATCTCTG	540
QY	601	GAGGCGGTGGCGTATTTGGCACTCACTCAATGATGTGACAGGAATCTCAAGCTGGAGAC	660
Db	541	GAGGCGGTGGCGTATTTGGCACTCACTCAATGATGTGACAGGAATCTCAAGCTGGAGAC	600
QY	661	CTGGTTTACTACAAACCGGCTGAAGAACTCCAGATTTGTCTCATGTGACTTCTGAGCT	720
Db	601	CTGGTTTACTACAAACCGGCTGAAGAACTCCAGATTTGTCTCATGTGACTTCTGAGCT	660
QY	721	AACTTAAGAAAATGAGCTTCATCAAGAGCCCTGTGGGACCCCCGAGTATCTG-----	771
Db	661	AACTTAAGAAAATGAGCTTCATCAAGAGCCCTGTGGGACCCCCGAGTATCTGAGCAAGAC	720
QY	772	-----	771
Db	721	GGGGTGGGGGCAAGGGGAGGAGATATAGGGGAGCAGCTTCAGGGAGCTGCTTGGGCAAG	780
QY	772	-----	771
Db	781	GGGAAAAATGTCTCATCTCAGAGAGTGGTGTGGATGTGATCTGAGACTGAGCTGAGGCTG	840
QY	772	-----GCCCAAGAGTGGTAGGCGCGGAGCGGT	799
Db	841	ATACTGACCAAGAGATGGGGCGTGTGTGTGAGGCCAGAGGTGTAGGCGCGGAGCGGT	900
QY	800	ATGGAAGCGCTGTGGAATGCTGGGCCATTGGAATCATCATGTACTACTT-----	848
Db	901	ATGGAAGCGCTGTGGAATGCTGGGCCATTGGAATCATCATGTACTACTTGTGATGTGACA	960
QY	849	-----	848
Db	961	GATGGACAGCAGGCTTGCACTCAGATGGGATGGGGCAATGTGTCTGTGGCTTCTGTG	1020
QY	849	-----GCTTCAGAGCAATCCACTTCTCTATGAGAGGTGGAGAG	889
Db	1021	TGAGCCCTTCCCCATGAGGCTTTCAGGCAACCCACTTCTCTATGAGAGGTGGAGAG	1080
QY	890	ATGATATATGAAACCATGATPAAGATCTCTTCGCAAGATCTGGCTGTGTGACTATGAT	949
Db	1081	ATGATATATGAAACCATGATPAAGATCTCTTCGCAAGATCTGGCTGTGTGACTATGAT	1140
QY	950	TTGACTCTCCATATTTGGGATGATATTTTCGAGAGCAGCAAGAGCTGGTACAAAGCTGA	1009
Db	1141	TTGACTCTCCATATTTGGGATGATATTTTCGAGAGCAGCAAGAGCTGGTACAAAGCTGA	1200
QY	1010	TGAGAGTGGAGCAAGACCAAGCGGATCACTCAGAGAGGCGCATCTCCATGAGTGATTT	1069
Db	1201	TGAGAGTGGAGCAAGACCAAGCGGATCACTCAGAGAGGCGCATCTCCATGAGTGATTT	1260
QY	1261	CTGGCAATGCTGCTTCTGATPAAGACATCAAGATGTGTGCTGTGCCAATTTGAANA	1320
Db	1321	ACTTTGCGAGGCGCAATGTGAGAGAGGCTGTCCGAGTGAACCACTTCATATAAGCGCTCC	1380
QY	1190	GGGACACAGAGCAGTCCAGACCGGCTGACGCCCAAGTGGGCTCAGCCACAGACACTGCCA	1249
Db	1381	GGGACACAGAGCAGTCCAGACCGGCTGACGCCCAAGTGGGCTCAGCCACAGACACTGCCA	1440
QY	1250	CCCCCGGGGCTGAGTGTGGGCCCAAGCTCAGCTGCGAGTGAAGTACTCACTCAAGCCCTG	1309

; CURRENT FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 1104
 ; SOFTWARE: pc_files Version 1.0
 ; SEQ ID NO: 19
 ; LENGTH: 2747
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (206)..(1618)
 ; US-10-037-270-19

Query Match 83.1%; Score 2595.2; DB 15; Length 2747;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 2700; Conservative 0; Mismatches 3; Indels 93; Gaps 1;

QY 50 TGCTGGAAGTCTGGTACGCGGAGGCGGCTGATCGGCGCGCGCTGCGCGGCTGCG 109
 DB 45 TGCTGGAAGTCTGGTACGCGGAGGCGGCTGATCGGCGCGCGCTGCGCGGCTGCG 104
 QY 110 GAGCGGATTTCTGCGCGCGCTGCGCGGAGCGCTGCGCGCGCGCTGAGCGCGCTGCACTT 169
 DB 105 GAGCGGATTTCTGCGCGCGCTGCGCGGAGCGCTGCGCGCGCGCTGAGCGCGCTGCACTT 164
 QY 170 CCTCCCTGTGACCAACCGCGCGCTGCAAGGTTAGAGCTTGGCAATCGCGTTTGGGTGTGA 229
 DB 165 CCTCCCTGTGACCAACCGCGCGCTGCAAGGTTAGAGCTTGGCAATCGCGTTTGGGTGTGA 224
 QY 230 CTCTGGGCGCAAGAACTATTAACCAAGCCATCGAGGTGATCTGAACAGATATGATTGG 289
 DB 225 CTCTGGGCGCAAGAACTATTAACCAAGCCATCGAGGTGATCTGAACAGATATGATTGG 284
 QY 290 GACAGGTATCAAGACTGAGGAGGTTTGTGAATCTTCCGGGCGCAAGGACCAAGCGACG 349
 DB 285 GACAGGTATCAAGACTGAGGAGGTTTGTGAATCTTCCGGGCGCAAGGACCAAGCGACG 344
 QY 350 GCAAGCTGCACACCTGCAAGAGTTCCAGAAGCGGAGCGCGCGCAAGGTTGGGAAAGCTG 409
 DB 345 GCAAGCTGCACACCTGCAAGAGTTCCAGAAGCGGAGCGCGCGCAAGGTTGGGAAAGCTG 404
 QY 410 CCAAGAACGAGATAGGCACTCTCAAGATGTGAAGCATCCCAACATCTTACAGCTGTGG 469
 DB 405 CCAAGAACGAGATAGGCACTCTCAAGATGTGAAGCATCCCAACATCTTACAGCTGTGG 464
 QY 470 ATGTGTTGTGACCCGCAAGAGTACTTATCTTCTGAGACTGGCCACGGGGAGGAGG 529
 DB 465 ATGTGTTGTGACCCGCAAGAGTACTTATCTTCTGAGACTGGCCACGGGGAGGAGG 524
 QY 530 TGTGTAATGATCTGTGACCAAGGCTACTACTCGAGGCGAGACCAAGCAAGCTGTGAC 589
 DB 525 TGTGTAATGATCTGTGACCAAGGCTACTACTCGAGGCGAGACCAAGCAAGCTGTGAC 584
 QY 590 GGAAGTCTGGAAGCGCGTGTGCTATTTGCACTCACTCAAGATCGTGACAGATCTCA 649
 DB 585 GGAAGTCTGGAAGCGCGTGTGCTATTTGCACTCACTCAAGATCGTGACAGATCTCA 644
 QY 650 AGCTGGAACCTGTGTTACTACACCGGCTGGAAGACTCGAAGATTGTCACTGTAAT 709
 DB 645 AGCTGGAACCTGTGTTACTACACCGGCTGGAAGACTCGAAGATTGTCACTGTAAT 704
 QY 710 TCCATCTGCTTAAGTAAAGATGCTTCATCAAGAGACCTGTGGAGCCCCCGAGATC 769
 DB 705 TCCATCTGCTTAAGTAAAGATGCTTCATCAAGAGACCTGTGGAGCCCCCGAGATC 764
 QY 770 TGGCCCCAGAGGTGTAGAGCGGAGCGGTATGAGCGCCGTGTGAGCTGTGGCCATTTG 829
 DB 765 TGGCCCCAGAGGTGTAGAGCGGAGCGGTATGAGCGCCGTGTGAGCTGTGGCCATTTG 824
 QY 830 GAGTCATCATGTACATCTGCTTTTCAGGCAATCCACTTTCTATGAGAGGTGGAAGAG 889

DB 825 GAGTCATCATGTACATCTGCTTTTCAGGCAATCCACTTTCTATGAGAGGTGGAAGAG 884
 QY 890 ATGATTATGAGAACCATGATTAAGATCTTCCGAGATCCGTGCTGTGATGATAGT 949
 DB 885 ATGATTATGAGAACCATGATTAAGATCTTCCGAGATCCGTGCTGTGATGATAGT 944
 QY 950 TTGACTCTTCATATTGGGATGATATTTCGAGGCGCAAGCAAGCTGTGATGAGGCTGA 1009
 DB 945 TTGACTCTTCATATTGGGATGATATTTCGAGGCGCAAGCAAGCTGTGATGAGGCTGA 1004
 QY 1010 TGGAGGTGAGCAAGACCGAGGATCACTGCAAGAAAGAGCCATCTCCATGATGATTT 1069
 DB 1005 TGGAGGTGAGCAAGACCGAGGATCACTGCAAGAAAGAGCCATCTCCATGATGATTT 1064
 QY 1070 CTGGCAATGCTGCTCTGATTAAGAACATCAAGAGATGTGTCTGTGCCAGATTGAAAAGA 1129
 DB 1065 CTGGCAATGCTGCTCTGATTAAGAACATCAAGAGATGTGTCTGTGCCAGATTGAAAAGA 1124
 QY 1130 ACTTTGCCAGGCGCAAGTGAAGAGGCTGTCCAGTGAACCACTCTCATGAAGCGGCTCC 1189
 DB 1125 ACTTTGCCAGGCGCAAGTGAAGAGGCTGTCCAGTGAACCACTCTCATGAAGCGGCTCC 1184
 QY 1190 GGGCAACAGAGAGTTCAGACAGGCTGACAGCCAGTCCGCTCAGCCACAGACTGCCA 1249
 DB 1185 GGGCAACAGAGAGTTCAGACAGGCTGACAGCCAGTCCGCTCAGCCACAGACTGCCA 1244
 QY 1250 CCCCAGGAGCTGCAAGTGGAGGCCACAGCTGCAAGTGGAGTCACTAGCCCTTG 1309
 DB 1245 CCCCAGGAGCT----- 1255
 QY 1310 AGGGTATGCTGCTGTGCTGCAAGAGATGATATGTGAGCCCGCCAGACCGTAGTGCA 1369
 DB 1256 -----GAGACCGTAGTGCA 1271
 QY 1370 CCCCAAGCAGATGGAATGTCACCCAGCCACTGATGCGAGTGCACCCAGCGACCG 1429
 DB 1272 CCCCAAGCAGATGGAATGTCACCCAGCCACTGATGCGAGTGCACCCAGCGACCG 1331
 QY 1430 ATGGAAGCATCTCCAGCCACTGATGGAAGTGTCACTCCAGTCACTGACAGAGCGCTA 1489
 DB 1332 ATGGAAGCATCTCCAGCCACTGATGGAAGTGTCACTCCAGTCACTGACAGAGCGCTA 1391
 QY 1490 CTCACGCCATGATGGAAGAGCCACACGAGCCACAGAAAGAGCATGTGGCCACACCC 1549
 DB 1392 CTCACGCCATGATGGAAGAGCCACACGAGCCACAGAAAGAGCATGTGGCCACACCC 1451
 QY 1550 AAAAGAGTGCATGCTGGGCGACCAAGGCGAGTGCACCCCTGAGCGGCTATGCGCCAGC 1609
 DB 1452 AAAAGAGTGCATGCTGGGCGACCAAGGCGAGTGCACCCCTGAGCGGCTATGCGCCAGC 1511
 QY 1512 CGGACAGCAGAGGCCCGACAGGCGCGCACAGCGCAGGCTCACTCTAGTAAAGGGGAAG 1571
 DB 1670 AGGCTGCTGTTATGCGCCAGAGTCTCAAGGGAGAGGCGCAGCTGATGAGGAGCTGG 1729
 QY 1572 AGGCTGCTGTTATGCGCCAGAGTCTCAAGGGAGAGGCGCAGCTGATGAGGAGCTGG 1631
 DB 1730 TGAAGGGGGGCGAGGAGTGGGAGAGGAGTGGGAGTGGAGTGGAGGGCTTCTCACTGTA 1789
 QY 1632 TGAAGGGGGGCGAGGAGTGGGAGAGGAGTGGGAGTGGAGTGGAGGGCTTCTCACTGTA 1691
 DB 1790 CATAGAGTCACTGAGCATGATGCTGCTCCCGCATGCCCCCATATCCCATGAGGAGATA 1849
 QY 1692 CATAGAGTCACTGAGCATGATGCTGCTCCCGCATGCCCCCATATCCCATGAGGAGATA 1751
 DB 1850 ACTAGAGGATCACGAGAGAGCAATCTGCTGCTGTGTGTATGTGTGATGTGTGAGGAG 1909
 QY 1752 ACTAGAGGATCACGAGAGAGCAATCTGCTGCTGTGTGTATGTGTGATGTGTGAGGAG 1811
 DB 1910 GCCAGTGGCAGGGGCGGCGCCAGCCCGCTGATGATCTTGTGGCTTTTCTGCTTTTG 1969

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us-10-669-689-1.rnpb

Page 16

Db	1812	GCGAGTGGCAGAGGGCCGGGCCCGACGCCCTGCATGGATTCTGTGGCTTTCTTGCTCTTTGG	1.871
QY	1970	CTAGCTTACACACAGTTTCTGTTCCTTGTGGGATGTGCTCTTAGGGATTACTCAGAGGGGCTCC	2029
Db	1872	CTAGCTTACACAGTTTCTGTTCCTTGTGGGATGTGCTCTTAGGGATTACTCAGAGGGGCTCC	1931
QY	2030	TGCTCTCTTCCCCCTTCCCTTCTTGCCCTCAATTCCTCCAGGAGGCCCTGCAGAGTCCC	2089
Db	1932	TGCTCTCTTCCCCCTTCCCTTCTTGCCCTCAATTCCTCCAGGAGGCCCTGCAGAGTCCC	1991
QY	2090	ACACTCTCCAGAGCCCTAAACTTTGGGCGGCTTCCCTCGAGAGCTGTGCTCCAGCGAGG	2149
Db	1992	ACACTCTCCAGAGCCCTAAACTTTGGGCGGCTTCCCTCGAGAGGTGTGCTCCAGCGAGG	2051
QY	2150	CCCTGTACGGGTCTTAGCTAGCTCTGCACATGAAAGTGTGTGCTGTGTGTGGGCTGC	2209
Db	2052	CCCTGTACGGGTCTTAGCTAGCTCTGCACATGAAAGTGTGTGCTGTGTGTGGGCTGC	2111
QY	2210	TCTTAGGACGAAATACAGGCTGTATTAGATGAGATGAGAAAGGTAGGGACGATATGTTAAGT	2269
Db	2112	TCTTAGGACGAAATACAGGCTGTATTAGATGAGATGAGAAAGGTAGGGACGATATGTTAAGT	2171
QY	2270	CCAGACTTTGGCACAATGGCTAGGATATACGTCTCATAGCTGTGAGAGTCTCAGAGATGGA	2329
Db	2172	CCAGACTTTGGCACAATGGCTAGGATATACGTCTCATAGCTGTGAGAGTCTCAGAGATGGA	2231
QY	2330	GAGAAATGATAGAGAGGCGAAGAGTCCATTTTGTCTCTTCTTAAAGACCTGTATTTGT	2389
Db	2232	GAGAAATGATAGAGAGGCGAAGAGTCCATTTTGTCTCTTCTTAAAGACCTGTATTTGT	2291
QY	2390	GTATTATTCCTGCTCTTCCGAGTCTCTGCAGTGGGCTGCCCTGTACCTCTGAACCTCATAGGC	2449
Db	2292	GTATTATTCCTGCTCTTCCGAGTCTCTGCAGTGGGCTGCCCTGTACCTCTGAACCTCATAGGC	2351
QY	2450	CTCTTAGGGGAAGAAGGAAACAATTAGAGCTGTGCATATAGACTGTGCAGGGCAGAGTACA	2509
Db	2352	CTCTTAGGGGAAGAAGGAAACAATTAGAGCTGTGCATATAGACTGTGCAGGGCAGAGTACA	2411
QY	2510	AGCCAGAGACCCAGTGTCCAGACCCTTACTGTGGTCTCTTACCCTGTGGCCAAACAGGAGGGC	2569
Db	2412	AGCCAGAGACCCAGTGTCCAGACCCTTACTGTGGTCTCTTACCCTGTGGCCAAACAGGAGGGC	2471
QY	2570	TGATPACTCTTGTCTCTTCTTAGATGCCAAGCTCTTAACAATCTCAGCCCAACAATGCTCTCT	2629
Db	2472	TGATPACTCTTGTCTCTTCTTAGATGCCAAGCTCTTAACAATCTCAGCCCAACAATGCTCTCT	2531
QY	2630	CCACCCCTAGGGGGCTTGTCTGCATGGCAATPACTCAATATCTGATTTGAGAGTTTGCCTT	2689
Db	2532	CCACCCCTAGGGGGCTTGTCTGCATGGCAATPACTCAATATCTGATTTGAGAGTTTGCCTT	2591
QY	2690	TACAGGGGCAAGATTTTCTGTCTCAGTTCAACATGAATGAAGAGAGACTCCCTCTTTCTTA	2749
Db	2592	TACAGGGGCAAGATTTTCTGTCTCAGTTCAACATGAATGAAGAGAGACTCCCTCTTTCTTA	2651
QY	2750	CAGCTCACTTCTATCAGAGGCCCAGAGTGCCTCAGAGCCACATTTGATGCTTTTCTGGG	2809
Db	2652	CAGCTCACTTCTATCAGAGGCCCAGAGTGCCTCAGAGCCACATTTGATGCTTTTCTGGG	2711
QY	2810	ATGAGGAAGTAGGGTTAAACTCCCAAGTTTCTGTAG	2845
Db	2712	ATGAGGAAGTAGGGTTAAACTCCCAAGTTTCTGTAG	2747

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RESULT 10
US-10-117-722-19
; Sequence 13, Application US/101177222-19
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Dimaenc, Radoje T.

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	TITLE OF INVENTION:	No.	US2003029744A1el	Nucleic Acids and
	TITLE OR INVENTION:	Polypeptides		
	FILE REFERENCE:	784CIP2BCIP		
	CURRENT APPLICATION NUMBER:	US/10/117,722		
	CURRENT FILING DATE:	2002-04-04		
	PRIOR APPLICATION NUMBER:	09/620,312		
	PRIOR FILING DATE:	2000-07-19		
	PRIOR APPLICATION NUMBER:	09/552,317		
	PRIOR FILING DATE:	2000-04-25		
	PRIOR APPLICATION NUMBER:	09/488,725		
	PRIOR FILING DATE:	2000-01-21		
	NUMBER OF SEQ ID NOS:	1104		
	SOFTWARE:	pt_fl_genes Version 1.0		
	SEQ ID NO 19			
	LENGTH:	2747		
	TYPE:	DNA		
	ORGANISM:	Homo sapiens		
	FEATURE:			
	NAME/KEY:	CDS		
	LOCATION:	(206)..(1618)		
	US-10-117-722-19			
	Query Match	83.1%; Score 2595.2;	DB 16;	Length 2747;
	Best Local Similarity	96.6%;	Pred. No. 0;	
	Matches 2700;	Conservative 0;	Mismatches 3;	Indels 93; Gaps 1;
OY	50	TGCTGAGAGTTCCGTACGCCGAAGCGCTGCATCTGGCGCCGCTCTGCCCCGCTGCTCG	109	
Db	45	TGCTGAGAGTTCCGTACGCCGAAGCGCTGCATCTGGCGCCGCTCTGCCCCGCTGCTCG	104	
OY	110	GAGCGAATTTCGCCCGCGTCCCAGGACCCTCGCGCCCGCTGAGCCGCATCACTT	169	
Db	105	GAGCGAATTTCGCCCGCGTCCCAGGACCCTCGCGCCCGCTGAGCCGCATCACTT	164	
OY	170	CCTCCCTGTGACCAACCGCGCTGCAGATTAGAAGCTTGCAATSCCGTTTGGTGTGTGA	229	
Db	165	CCTCCCTGTGACCAACCGCGCTGCAGATTAGAAGCTTGCAATSCCGTTTGGTGTGTGA	224	
OY	230	CTCTGGCGCACAGAAAGACTATAACAGCATTCGAGGTGACTGACAGATATGATTTGG	289	
Db	225	CTCTGGCGCACAGAAAGACTATAACAGCATTCGAGGTGACTGACAGATATGATTTGG	284	
OY	290	GACAGGTTCATCAAGACTGAGGAGTTTGTAAATCTTCCSGGCCAAGACAAGACGACG	349	
Db	285	GACAGGTTCATCAAGACTGAGGAGTTTGTAAATCTTCCSGGCCAAGACAAGACGACG	344	
OY	350	GCAAGCTGCACACCTGCAGAAAGTTCCAGAACGCGGACGCGGACAGGTGCGAAAAGCTG	409	
Db	345	GCAAGCTGCACACCTGCAGAAAGTTCCAGAACGCGGACGCGGACAGGTGCGAAAAGCTG	404	
OY	410	CGAAGACAGATNAGGCACTCTCAAGATGTGGAAGCATCCCAACATCTTAACAGCTGTGG	469	
Db	405	CGAAGACAGATNAGGCACTCTCAAGATGTGGAAGCATCCCAACATCTTAACAGCTGTGG	464	
OY	470	ATGTGTTGTGTAACCGCGAAGAGTAATTTATCTTCTGTGAGCTGGCCACGGGAGAGGAG	529	
Db	465	ATGTGTTGTGTAACCGCGAAGAGTAATTTATCTTCTGTGAGCTGGCCACGGGAGAGGAG	524	
OY	530	TGTTTGACTGATCCTTGACCAAGGCTTACTCTGGAACGAGACAACAAGCAACTGTGTAC	589	
Db	525	TGTTTGACTGATCCTTGACCAAGGCTTACTCTGGAACGAGACAACAAGCAACTGTGTAC	584	
OY	590	GCGAAGTCTTGAGAGCGCTGTGCTTATTTGCACTCACTCAAGATCTGTGACAGGAATCTCA	649	
Db	585	GCGAAGTCTTGAGAGCGCTGTGCTTATTTGCACTCACTCAAGATCTGTGACAGGAATCTCA	644	
OY	650	AGCTGGAACACTGTGTTTACTACACCGGCTGAGAACTTCGAAGATTGTCACTCACTGACT	709	
Db	645	AGCTGGAACACTGTGTTTACTACACCGGCTGAGAACTTCGAAGATTGTCACTCACTGACT	704	
OY	710	TCATCTGTGCTAAGCTAGAAAAATGCGCTCATCAAGAGACCTGTGGAGACCCCGAGTATC	769	
Db	705	TCATCTGTGCTAAGCTAGAAAAATGCGCTCATCAAGAGACCTGTGTGGAGACCCCGAGTATC	764	


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/ GENERAL INFORMATION:
/ APPLICANT: Olandt, Peter J.
/ APPLICANT: Kapeller-Libermann, Rosana
/ TITLE OF INVENTION: 2504, 1597, AND 14760, NOVEL PROTEIN
/ TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
/ FILE REFERENCE: 10448-017001
/ CURRENT APPLICATION NUMBER: US/09/797,039
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: US 60/186,061
/ PRIOR FILING DATE: 2000-02-29
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2297
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (154)...(1656)
/ NAME/KEY: misc feature
/ LOCATION: (1)-(2297)
/ OTHER INFORMATION: n = A,T,C or G
/ US-09-797-039-1

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Query Match      73.1%; Score 2283.4; DB 9; Length 2297;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 68 CGAAGCGGTGATCTGGGCGCGCGTCTGCGCGCTGCTGCGAGCGATTCTGCGCGC 127
DB 11 CGAAGCGGTGATCTGGGCGCGCGTCTGCGCGCTGCTGCGAGCGATTCTGCGCGC 70
QY 128 GTCCCGCGAGCCCTCGGCGCGCGCTGAGCCCGCGCATCTTCTCTCCCTGTACCAACG 187
DB 71 GTCCCGCGAGCCCTCGGCGCGCGCTGAGCCCGCGCATCTTCTCTCCCTGTACCAACG 130
QY 188 GCGCTCAGGTTAGAGCTGGGCAATGCGGTTGGGTGTGACTCTGGGCGCAAGAGA 247
DB 131 GCGCTCAGGTTAGAGCTGGGCAATGCGGTTGGGTGTGACTCTGGGCGCAAGAGA 190
QY 248 ACTATAACAGCCATCGAGGTGATGACAGATATGATTGGGCAAGATCATCAAGCTG 307
DB 191 ACTATAACAGCCATCGAGGTGATGACAGATATGATTGGGCAAGATCATCAAGCTG 250
QY 308 AGAGATTGTTGAAATCTTCGGGCGCAAGAGCAAGACAGGCAAGCTGCACTGCA 367
DB 251 AGAGATTGTTGAAATCTTCGGGCGCAAGAGCAAGACAGGCAAGCTGCACTGCA 310
QY 368 AGAAGTTCCAGAACCGGAGCGCGCGCAAGGTGGGAAAGCTGCAAGACAGATAGGA 427
DB 311 AGAAGTTCCAGAACCGGAGCGCGCGCAAGGTGGGAAAGCTGCAAGACAGATAGGA 370
QY 428 TCTCAAGATGAGTGAAGCATCCCAACATCTTACAGCTGTGATGTGTTGTGACCGGA 487
DB 371 TCTCAAGATGAGTGAAGCATCCCAACATCTTACAGCTGTGATGTGTTGTGACCGGA 430
QY 488 AGAGATCTTATCTTCTGAGCTGGGCAAGGAGGAGGAGTGTGATGATGATCTG 547
DB 431 AGAGATCTTATCTTCTGAGCTGGGCAAGGAGGAGGAGTGTGATGATGATCTG 490
QY 548 ACCGAGGCTACTACTCGGAGCGAGACACAGCAAGCTGTGTAAGGCAAGTCTGAGCGG 607
DB 491 ACCGAGGCTACTACTCGGAGCGAGACACAGCAAGCTGTGTAAGGCAAGTCTGAGCGG 550
QY 608 TGGGCTATTGCACTCACTCAAGATGTGCAAGAGATCTCAAGCTGAGAGACCTGATT 667
DB 551 TGGGCTATTGCACTCACTCAAGATGTGCAAGAGATCTCAAGCTGAGAGACCTGATT 610
QY 668 ACTACAACCGGCTGAGAACTCGAAGATTGTCACTGATGATCTTCACTTGGCTAAGCTAG 727
DB 611 ACTACAACCGGCTGAGAACTCGAAGATTGTCACTGATGATCTTCACTTGGCTAAGCTAG 670
QY 728 AAAATGGCTTCATCAAGAGCCCTGTGGGACCCCGAGTATCTGGCCCCAGAGGTGATAG 787

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DB 671 AAAATGGCTTCATCAAGAGCCCTGTGGGACCCCGAGTATCTGGCCCCAGAGGTGATAG 730
QY 788 GCCGCGAGCGGTATGAGACGCCCTGTGAGATGCTGGGCAATGAGTCAATCATATGATACC 847
DB 731 GCCGCGAGCGGTATGAGACGCCCTGTGAGATGCTGGGCAATGAGTCAATCATATGATACC 790
QY 848 TGCCTTCAAGCAATCCACTTTCTATGAGAGGTGAGAGATGATATATGAGAACCATG 907
DB 791 TGCCTTCAAGCAATCCACTTTCTATGAGAGGTGAGAGATGATATATGAGAACCATG 850
QY 908 ATTAAGATCTTCTTCCGCAATCTGCTGTGTATCATATGAGTTGATCTCCATATTGGG 967
DB 851 ATTAAGATCTTCTTCCGCAATCTGCTGTGTATCATATGAGTTGATCTCCATATTGGG 910
QY 968 ATGATATTGCGAGGCGCAAGACCTGGTCACAAGGCTGATGAGTGGAGCAAGACC 1027
DB 911 ATGATATTGCGAGGCGCAAGACCTGGTCACAAGGCTGATGAGTGGAGCAAGACC 970
QY 1028 AGCGGATCACTGAGAGAGAGCCATCTCCCATGATGATGATTTGTGCAATGCTGTTCTG 1087
DB 971 AGCGGATCACTGAGAGAGAGCCATCTCCCATGATGATGATTTGTGCAATGCTGTTCTG 1030
QY 1088 ATTAAGATCAATAGATGTGTCTGTGCTGCTGCAATGAGAACTTTGCGAGGCGCAAGT 1147
DB 1031 ATTAAGATCAATAGATGTGTGTGTGCTGCTGCAATGAGAACTTTGCGAGGCGCAAGT 1090
QY 1148 GGAAGAAAGGTGTCCGAGTACCAACCCCTCATGAAAGGCTCGGAGGACCGAGAGATCCA 1207
DB 1091 GGAAGAAAGGTGTCCGAGTACCAACCCCTCATGAAAGGCTCGGAGGACCGAGAGATCCA 1150
QY 1208 GCACGGCTGCGAGCCATCGGCTGAGCGCAAGCACTGCGCAACCCCGGAGGTGCAAGTG 1267
DB 1151 GCACGGCTGCGAGCCATCGGCTGAGCGCAAGCACTGCGCAACCCCGGAGGTGCAAGTG 1210
QY 1268 GGGCCAGAGCTGAGCTGCGAGTGAAGCTACTGAGCCCTGAGAGGTGATGCTGCTGTG 1327
DB 1211 GGGCCAGAGCTGAGCTGCGAGTGAAGCTACTGAGCCCTGAGAGGTGATGCTGCTGTG 1270
QY 1328 CTGCAAGAGTGAATATGTGCCCCCGGCAAGCGGTATGCGCAACCCCGGAGGTGAGTGA 1387
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OY		1928	CCAGcCCcCTGcATGAgTTcCTTGTgGcCTTTCGTCTTGTgCTAgCTTCACAAGTTTC		1987
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OY		2048	CTTCCTGcCTCACCAATTCCcCTTAGGcAGGcCTTCAGTTCACAActTCCTCCAAGcCTTA		2107
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OY		2288	TAGGgATAcTGTCTAcTAgCTGTGTGAAGTTCCTCAGAGTGTGAGAA'TAgTAGAGAGggc		2347
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Sequence 18, Application US/10423543					
Publication No. US20040058355A1					
GENERAL INFORMATION:					
APPLICANT: Millennium Pharmaceuticals, Inc.					
APPLICANT: Libermann, Rosana K.					
APPLICANT: Hunter, John J.					
APPLICANT: Meyers, Rachel E.					
APPLICANT: Rudolph-Owen, Laura A.					
APPLICANT: Curtis, Rory A.J.					
APPLICANT: Olandt, Peter J.					
APPLICANT: Tsai, Feng-Ying					
APPLICANT: Galvin, Katherine M.					
APPLICANT: Chun, Miyoung					
APPLICANT: Williamson, Marx J.					
APPLICANT: Siles-Santiago, Inmaculada					
APPLICANT: Bandaru, Rajasekhar					
TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,					
TITLE OF INVENTION: 14760, 32501, 17903, 3700, 21529, 26175, 26343, 56638,					
TITLE OF INVENTION: 18610, 35211, 21986, h1983, m1983, 58555 OR 593 MOLECULES					
TITLE OF INVENTION: AND USE THEREFOR					
FILE REFERENCE: MPI03-023OMNIM					
CURRENT APPLICATION NUMBER: US/10/423,543					
CURRENT FILING DATE: 2003-04-25					
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PRIOR APPLICATION NUMBER: US 60/205,447					
PRIOR FILING DATE: 2000-05-19					
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PRIOR FILING DATE: 2001-11-13					
PRIOR APPLICATION NUMBER: US 60/248,325					

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US-10-423-543-18

Query Match          73.1%; Score 2283.4; DB 13; Length 2297;
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Matches 2284; Conservative 0; Mismatches 3; Indels 0; Gaps 0

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QY      128  GTCGCCGAGCCCTCGGCGCCCGCTGAGCCCGGATCACTTCCTCCGTGCAACCG 187
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QY      188  GCGCTGCAAGTTAGAGCTGCGCAATGCGCTTTGGGTGTGACTCTGGCGCAAGAGAGA 247
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QY      248  ACTATTAACCAAGCCATCGSAGGTGACTGAAGATATGATTTGGACAGGTGATCAAGACTG 307
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QY      308  AGAAGTTTGTGAAATCTTCCGGGCGCAAGAGCAAGACAGGCAAGCTGCACACTGCA 367
Db      251  AGAAGTTTGTGAAATCTTCCGGGCGCAAGAGCAAGAGCAAGGCAAGCTGCACACTGCA 310

QY      368  AGAAGTTCCAGAGCGGAGCGCGCAAGGTGCGGAAAGCTGCCAAGAAAGATAGCA 427
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QY      428  TCCTCAAGATGSGTAGAGCATCCCAACATCTTACAGCTGTGTGATGTGTGATCCCGCA 487
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QY      488  AGAAGTACTTTATCTTCTGAGAGCTGCGCACCGGGAAGAGAGGTGTGACTGGAATCTGCG 547
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QY      548  ACCAGAGGCTACTACTCGSAGCGAGACCAAGCAACGTGTATACGGAAGCTTGGAAGCCG 607
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Db      551  TGGCTATTATGGACTCACTCAAGATCGTGCAAGAGAACTCAAGCTTGAGAACTTGATTT 610

QY      668  ACTACACCGGCTGAAGAACTCGAAGATTGTCATCATGATCTTCATCTGGCTAACTGAG 727

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PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: PCT/US01/16549
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/801,267
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: PCT/US01/07138
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/187,454
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PRIOR APPLICATION NUMBER: US 09/829,671
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: PCT/US01/40483
PRIOR FILING DATE: 2001-04-11
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PRIOR FILING DATE: 2000-04-18
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PRIOR FILING DATE: 2001-09-24
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PRIOR FILING DATE: 2001-09-24
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PRIOR FILING DATE: 2000-09-25
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PRIOR APPLICATION NUMBER: US 60/246,561
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PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/187,420
PRIOR FILING DATE: 2000-03-07
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SEQ ID NO: 1
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (154)..(1656)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(2297)
OTHER INFORMATION: n = A,T,C or G
US-10-170-789-1

Query Match 73.1%; Score 2283.4; DB 15; Length 2297;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 11 CCAAGCGGTGATCTGGGCGCGGCTTGCCCCGGTGTGCGAGCGGATTTCTGCCGCC 70
QY 128 GTCCCGGAGCGCTGGGCGCGGCGGCGGAGCGCGGATCACTTCCCTCCGTGACCAACG 187
DB 71 GTCCCGGAGCGCTGGGCGCGGCGGCGGAGCGCGGATCACTTCCCTCCGTGACCAACG 130
QY 188 GCGCTGAGGTAGAGCTGCAATGCGTTGGTGTGTGACTGTGGGCGCAAGAAGA 247
DB 131 GCGCTGAGGTAGAGCTGCAATGCGTTGGTGTGTGACTGTGGGCGCAAGAAGA 190
QY 248 ACTATTAACCAAGCATGAGGTGAGTGAAGATGATGATTTGGAGCAAGTCAAGACTG 307
DB 191 ACTATTAACCAAGCATGAGGTGAGTGAAGATGATGATTTGGAGCAAGTCAAGACTG 250
QY 308 AGAAGTTTGTGAATCTTCCGGGCGCAAGACAAAGCAAGCAAGCAAGTCAAGTCA 367

DB 251 AGAAGTTTGTGAATCTTCCGGGCGCAAGACAAAGCAAGCAAGCAAGTCAAGTCA 310
QY 368 AGAAGTTCCAGAACCGGAGCGCGCGAGAGTGGAGAAAGCTGCCAGAAAGATAGGA 427
DB 311 AGAAGTTCCAGAACCGGAGCGCGCGAGAGTGGAGAAAGCTGCCAGAAAGATAGGA 370
QY 428 TCCTCAAGATGGTGAAGCATCCCAATCCTTACAGCTGTGTGATGTTTGTGACCCGA 487
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Thu Apr 29 08:44:17 2004

us-10-669-689-1.rnpb

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? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: PT232
? CURRENT APPLICATION NUMBER: US/09/764,868
? CURRENT FILING DATE: 2001-01-17
? Prior application data removed - refer to PALM or file wrapper
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Dp	2369	CTGATGGAGTGTATACCCCACTCACTACAGAGACGTACTCCAGCCACTGATGGAGAG	2310						
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1829 CTTGTGGAGATGCTGCTCTAGAGAACTCAGAGGGGCTCTGCTCTCCCTCCCTTCCCTT 1770
2051 CTTGCTCACCATTCCCTTAGAGAGGCTCTGAGAGTCCCACTCTCCCAAGCCCTTAAC 2110
1769 CTTGCTCACCATTCCCTTAGAGAGGCTCTGAGAGTCCCACTCTCCCAAGCCCTTAAC 1710
2111 TTGGGCGGCTCTGCTCTAGAGAGTCTCTGAGAGGCTCTGAGAGGCTCTTAAAGCT 2170
1709 TTGGGCGGCTCTGCTCTAGAGAGTCTCTGAGAGGCTCTGAGAGGCTCTTAAAGCT 1650
2171 CTTGAGACATGAGAGTCTGCTCTGAGAGGCTCTGAGAGGCTCTTAAAGCT 2230
1649 CTTGAGACATGAGAGTCTGCTCTGAGAGGCTCTGAGAGGCTCTTAAAGCT 1590
2231 GTATGAGAGATGAGAGAGTAGGAGATGATGTTAATGTTAAGTCCAGATTGAGAGCTAG 2290
1589 GTATGAGAGATGAGAGAGTAGGAGATGATGTTAATGTTAAGTCCAGATTGAGAGCTAG 1530
2291 GGATGAGTCTCACTAGCTGAGAGTCTCTGAGAGTGAAGAAAGTGAAGAGGAGAGA 2350
1529 GGATGAGTCTCACTAGCTGAGAGTCTCTGAGAGTGAAGAAAGTGAAGAGGAGAGA 1470
2351 AGCTTCCATTTTGTCTCTCTAGAGACCTGTTAATTTGTATTCTCTGCTTCCGAG 2410
1469 AGCTTCCATTTTGTCTCTCTAGAGACCTGTTAATTTGTATTCTCTGCTTCCGAG 1410
2411 TCTGAGATGAGAGTCTGCTCTAGAGACCTCTGAGAGCTCTGAGAGAGAGAGAGAGA 2470
1409 TCTGAGATGAGAGTCTGCTCTAGAGACCTCTGAGAGCTCTGAGAGAGAGAGAGA 1350
2471 ATTAGAGATGAGAGATGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAG 2530
1349 ATTAGAGATGAGAGATGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAG 1280
2531 GCCTTACTGAGTCTCTTACCTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAG 2590
1289 GCCTTACTGAGTCTCTTACCTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAG 1230
2591 AGATGCCACCTCTCTCACTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 2650
1229 AGATGCCACCTCTCTCACTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 1171
2651 ATGGAATTAATCTAATCTGATTTGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 2710
1170 ATGGAATTAATCTAATCTGATTTGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 1111
2711 CAGTTCAACATGAAATGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAG 2770
1110 CAGTTCAACATGAAATGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAG 1051
2771 CAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 2830
1050 CAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 991
2831 CCCCAGTTTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 2890
990 CCCCAGTTTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTG 931
2891 GATAGGAGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAG 2950
930 GATAGGAGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAG 871
2951 CCGTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAG 3010
870 CCGTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAG 811
3011 CTGAACCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAG 3045
810 CTGAACCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAGAGTCTCTGAGAG 776

RESULT 15
US-10-669-689-3
; Sequence 3, Application US/10669689
; Publication No. US20040038363A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000612DIV1
; CURRENT APPLICATION NUMBER: US/10/669,689
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-689-3
Query Match 60.1%; Score 1876.6; DB 13; Length 7542;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
1151 AGAAGGCTGCTCCGAGAGTACACCTCATGAAAGGCTCCGGGACACAGAGAGTCCAGCA 1210
3979 AGAAGGCTGCTCCGAGAGTACACCTCATGAAAGGCTCCGGGACACAGAGAGTCCAGCA 4038
1211 CGGCTCAGACCCAGTGTGGCTCTGAGCAGACACTGCCACCCCGGGGCTGAGGTGGG 1270
4039 CGGCTCAGACCCAGTGTGGCTCTGAGCAGACACTGCCACCCCGGGGCTGAGGTGGG 4098
1271 CCAGAGCTGAGCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1330
4099 CCAGAGCTGAGCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 4158
1331 CAAGAGTATATGTGGGCCCCCGCAGACCTGATGACCCACCCAGCCAGTGAAGT 1390
4159 CAAGAGTATATGTGGGCCCCCGCAGACCTGATGATGACCCACCCAGTGAAGT 4218
1391 CCAAGGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1450
4219 CCAAGGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 4278
1451 CTGATGGAGTGTGACCCAGTCACTGAGAGAGGCTCTGAGAGAGTCTGAGAGAGTCTGAG 1510
4279 CTGATGGAGTGTGACCCAGTCACTGAGAGAGGCTCTGAGAGAGTCTGAGAGAGTCTGAG 4338
1511 CCAAGGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1570
4339 CCAAGGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 4398
1571 CCAAGGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1630
4399 CCAAGGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 4458
1631 GCGCCAGAGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1690
4459 GCGCCAGAGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 4518
1691 AGTCTCAAAGGAGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1750
4519 AGTCTCAAAGGAGAGAGTCTGAGTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 4578
1751 CAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1810
4579 CAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4638
1811 CCTGCTGCTCCCATGCTCCCATGCTCCCATGCTCCCATGCTCCCATGCTCCCATGCTCCCAT 1870

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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:46:04 ; Search time 20 Seconds

(Without alignments)
2409.598 Million cell updates/sec

Title: US-10-669-689-2

Perfect score: 2581

Sequence: 1 MPFGCVTLGDKKNYNQSEV.....SSKGEAGYAGQSGREAS 501

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2383.5	92.3	504	2	156542 calmodulin-binding
2	1537.5	59.6	421	2	156542 calmodulin-binding
3	797.5	30.9	374	1	550193 Ca2+/calmodulin-de
4	793	30.7	370	1	557347 Ca2+/calmodulin-de
5	713	27.6	348	2	137321 Ca2+/calmodulin-de
6	645.5	25.0	310	2	888640 protein K07A9.2 [i
7	620.5	24.0	474	1	137321 Ca2+/calmodulin-de
8	620.5	24.0	502	2	152637 Ca2+/calmodulin-de
9	608	23.6	473	1	153036 Ca2+/calmodulin-de
10	602.5	23.3	469	1	157656 Ca2+/calmodulin-de
11	552	21.4	542	1	155025 Ca2+/calmodulin-de
12	551	21.3	542	1	155025 Ca2+/calmodulin-de
13	545.5	21.1	589	2	155025 Ca2+/calmodulin-de
14	542	21.0	527	1	155025 Ca2+/calmodulin-de
15	535	20.7	556	2	155025 Ca2+/calmodulin-de
16	534	20.7	478	1	155025 Ca2+/calmodulin-de
17	529.5	20.5	414	2	155025 Ca2+/calmodulin-de
18	527.5	20.4	301	1	155025 Ca2+/calmodulin-de
19	521	20.2	335	2	155025 Ca2+/calmodulin-de
20	521	20.2	478	1	155025 Ca2+/calmodulin-de
21	517.5	20.1	533	1	155025 Ca2+/calmodulin-de
22	513.5	19.9	518	1	155025 Ca2+/calmodulin-de
23	512.5	19.9	518	1	155025 Ca2+/calmodulin-de
24	510.5	19.8	708	2	155025 Ca2+/calmodulin-de
25	509.5	19.7	509	2	155025 Ca2+/calmodulin-de
26	509.5	19.7	530	2	155025 Ca2+/calmodulin-de
27	502.5	19.5	516	1	155025 Ca2+/calmodulin-de
28	491.5	19.0	547	2	155025 Ca2+/calmodulin-de
29	491.5	19.0	554	2	155025 Ca2+/calmodulin-de

30	483.5	18.7	531	2	155025	probable calcium d
31	483.5	18.7	1423	1	137275	death-associated p
32	481.5	18.7	319	2	138138	protein-serine kin
33	481.5	18.7	540	1	101989	calcium-dependent
34	479.5	18.6	391	2	108722	protein R6A10.4 [
35	473	18.3	532	2	114335	protein kinase, ca
36	465	18.0	521	2	108583	calcium-dependent
37	465	18.0	1176	2	108583	calcium-dependent
38	463.5	18.0	1906	1	108583	calcium-dependent
39	462.5	17.9	387	1	108583	calcium-dependent
40	462	17.9	610	1	108583	calcium-dependent
41	462	17.9	1147	2	108583	calcium-dependent
42	461.5	17.9	538	2	108583	calcium-dependent
43	461	17.9	538	2	108583	calcium-dependent
44	460.5	17.8	490	2	108583	calcium-dependent
45	459.5	17.8	388	1	108583	calcium-dependent

ALIGNMENTS

RESULT 1

156542
calmodulin-binding protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C/Accession: 156542
R/Genbank: M. J. E. Brander, M. G. J. Hasel, K. W. J. Danielson, P. E. J. Wong, K. K. J. Battenberg, E. L. J. Neurosci. 14, 1-13, 1994
A/Title: 1G5: a calmodulin-binding, vesicle-associated, protein kinase-like protein enric
A/Reference number: 156542; PMID:94110847; PMID:8283228
A/Accession: 156542
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-504 <RES>

A/Keywords: 1G5: a calmodulin-binding, vesicle-associated, protein kinase-like protein enric
C/Keywords: calmodulin binding
F/22-286/Domain: protein kinase homology <KIN>

Query Match
Best Local Similarity 92.3%; Score 2383.5; DB 2; Length 504;
Matches 468; Conservative 5; Mismatches 23; Indels 13; Gaps 2;

QY	1	MPFGCVTLGDKKNYNQSEVTRDYLGVYKTEECCEIFRAKDCTTKLTKCKFOQRKDQ	60
DB	1	MPFGCVTLGDKKNYNQSEVTRDYLGVYKTEECCEIFRAKDCTTKLTKCKFOQRKDQ	60
QY	61	RKYRKAKNEIGILKKVKNPILQVDFVTRKEFIPIELATGREGVPMILDOGYSSR	120
DB	61	RKYRKAKNEIGILKKVKNPILQVDFVTRKEFIPIELATGREGVPMILDOGYSSR	120
QY	121	DTSNVROYLEAVAYHSLKIVRNKLENTVYRNKSKIVISDFHLAKLNGLKEP	180
DB	121	DTSNVROYLEAVAYHSLKIVRNKLENTVYRNKSKIVISDFHLAKLNGLKEP	180
QY	181	CGTPEYLAPEVVGROGVRPDCMAIGVMTYLLSGNPFYEVBEEDVDENDKLFRKI	240
DB	181	CGTPEYLAPEVVGROGVRPDCMAIGVMTYLLSGNPFYEVBEEDVDENDKLFRKI	240
QY	241	LAGDYEFDSPPYDDISQAAKDLVTRIMEVEDQRTTAEBAISHWISGNAASDKNIKGV	300
DB	241	LAGDYEFDSPPYDDISQAAKDLVTRIMEVEDQRTTAEBAISHWISGNAASDKNIKGV	300
QY	301	CAQIEKNPAPAKKKAQVNTTLMKRLAPQSGSTAAGASATDPATPAPAGATPAAS	360
DB	301	CAQIEKNPAPAKKKAQVNTTLMKRLAPQSGSTAAGASATDPATPAPAGATPAAS	360
QY	361	G-----ATSAPEGDARAKSDNVAPADRSATPATGSAATPATGSAATPATG	412
DB	361	G-----ATSAPEGDARAKSDNVAPADRSATPATGSAATPATGSAATPATG	412
QY	413	ATDGSVTPVTDGSAATPATGSAATPATGSAATPATGSAATPATGSAATPATG	472
DB	413	ATDGSVTPVTDGSAATPATGSAATPATGSAATPATGSAATPATGSAATPATG	472

Db 416 AHDGATVPATDTSATPATGRRATPATBESSTVPAQAASSAPAKAAATPEFAVACPDSTAL 475
 QY 473 EGATGQAPSSKGEAAGYAQESQREAS 501
 Db 476 EGATGQAPSSKGEAATGCQESQREAS 504

RESULT 2

T30814
 Calmodulin-binding protein kinase - Fugu rubripes
 C/Species: Fugu rubripes
 C/Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 03-Jun-2002
 C/Accession: T30814
 R/Cotage: A.J.; Clark, M.; Hawker, K.; Umanan, Y.; Wheller, D.; Bishop, M.; Elgar, G.
 FERS Lett. 443, 370-374, 1999
 A/Title: Three receptor genes for plasmalogen related growth factors in the genome of th
 A/Reference number: Z20880; MUID:9514833; PMID:10025966
 A/Accession: T30814
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1421 <COT>
 A/Cross-references: EMBL:AF010348; NID:e1355080; PID:e1355083; PIDN:CAA09101.1
 C/Genetic: 32/2; 76/2; 101/2; 147/3; 186/1; 211/2; 257/1; 283/2; 312/3

Query Match 59.6%; Score 1537.5; DB 2; Length 421;
 Best Local Similarity 76.2%; Pred. No. 1,5e-58;
 Matches 298; Conservative 36; Mismatches 42; Indels 15; Gaps 4;

QY 1 MPFGCVTLGPKKYNQSEVTDRLDQVITKEFECEIFPAKDKTGTGKLTCKKFGKRDG 60
 Db 1 MPFGCVTLGPKKYNQSEVTDRLDQVITKEFECEIFPAKDKTGTGKLTCKKFGKRDG 60
 QY 61 RYRKAANKIEGILKMYKHPNIIQLVDVFTREKEFIPELATGREVPMIIDQGYSSR 120
 Db 61 RYRKAANKIEGILKMYKHPNIIQLVDVFTREKEFIPELATGREVPMIIDQGYSSR 120
 QY 121 DTGNVVRQVLEAVAYVLSKTIHNRNLTENLVYNNRKNKSYISFHLAKENGILKEP 180
 Db 121 DTGNVVRQVLEAVAYVLSKTIHNRNLTENLVYNNRKNKSYISFHLAKENGILKEP 180
 QY 121 DTGNVVRQVLEAVAYVLSKTIHNRNLTENLVYNNRKNKSYISFHLAKENGILKEP 178
 Db 121 DTGNVVRQVLEAVAYVLSKTIHNRNLTENLVYNNRKNKSYISFHLAKENGILKEP 178
 QY 181 CGPEYVAPBVGQRGRPVDCATGVIMYIILSGNPPYEVEEDDVENHDKLFRKI 240
 Db 179 CGPEYVAPBVGQRGRPVDCATGVIMYIILSGNPPYEVEEDDVENHDKLFRKI 238
 QY 241 LAGDFEEDSEYMDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDG 300
 Db 239 LAGDFEEDSEYMDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDG 298
 QY 301 CAQIEKNFAPAKMKKAVRVTTLMLKRLAPQSSST-AAAGASAT-DTAPGAAGATAA 358
 Db 299 CAQIEKNFAPAKMKKAVRVTTLMLKRLAPQSSST-AAAGASAT-DTAPGAAGATAA 358
 QY 359 ASGATAPBEGDAAAASDNVAPADRSATPA 389
 Db 359 ASGATAPBEGDAAAASDNVAPADRSATPA 378

RESULT 3

S50193
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
 N/Alternate names: CamKI
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: S50193; A49682; A46038
 R/Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.
 Biochim. Biophys. Acta 1224, 156-160, 1994
 A/Title: Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent pro
 A/Reference number: S50193; MUID:95035115; PMID:7948088
 A/Accession: S50193
 A/Status: preliminary
 A/Molecule type: mRNA

A/Residues: 1-374 <CHO>
 A/Cross-references: EMBL:L26289; NID:9439613; PIDN:AAA66944.1; PID:9439614
 R/Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.
 J. Biol. Chem. 268, 26512-26521, 1993
 A/Title: Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification
 A/Reference number: A49682; MUID:9407534; PMID:8253780
 A/Accession: A49682

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-111, 'G', 113-117, 'R', 119-308, 'R', 310-322, 'HOPG', 327, 'T', 329, 'TDS' <PIC>
 A/Cross-references: GB:L24907; NID:9406112; PIDN:AAA19670.1; PID:9406113
 R/Mochizuki, H.; Ito, T.; Hidaka, H.
 J. Biol. Chem. 268, 9143-9147, 1993
 A/Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase V
 A/Reference number: A46038; MUID:93232082; PMID:8386178
 A/Accession: A46038
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 12-36, 'T' <MOC>
 A/Experimental source: cerebrium
 A/Note: sequence extracted from NCBI backbone (NCBI:129927)
 C/Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
 C/Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
 F/16-34/Domain: protein kinase homology <KIN>
 F/26-34/Region: protein kinase ATP-binding motif
 F/293-299/Region: autoinhibitory
 F/302-314/Region: calmodulin binding
 F/177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 30.9%; Score 797.5; DB 1; Length 374;
 Best Local Similarity 41.9%; Pred. No. 2.5e-27;
 Matches 160; Conservative 73; Mismatches 128; Indels 21; Gaps 4;

QY 14 YNQSSEVTDRLDQVITKEFECEIFPAKDKTGTGKLTCKKFGKRDGRKAKKNEIGI 73
 Db 10 WKQAEIDRIDYDFRDVGTGAFSEVILAEDEKTKLVAICIAKAKLEGKSGENSEIAV 69
 QY 74 LKMYKHPNIIQLVDVFTREKEFIPELATGREVPMIIDQGYSSRDTGNVVRQVLEAV 133
 Db 70 LKMYKHPNIIQLVDVFTREKEFIPELATGREVPMIIDQGYSSRDTGNVVRQVLEAV 129
 QY 134 AYLSKTIHNRNLTENLVYNNRKNKSYISFHLAKENGILKEP 191
 Db 130 KYLHDLGIVHDLKPENLVYSLDESKIMSDGLKMEDEPGVSLTAGCTPGYVAPEV 189
 QY 192 VGRQRYGPRVDCAIGVIMYIILSGNPPYEVEEDDVENHDKLFRKI 251
 Db 190 LAQKPYSKAVDCWSIGVAYIILGYPPEYDE-----NDATLFGQILKAEYEPDSPY 241
 QY 252 WDDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDG 311
 Db 242 WDDISQAADLVTRLMVEQDORITAEAIISHEMISGNAASDKNIKDG 301
 QY 312 KWKKAVRVTTLMLKRLAPQSSST-AAAGASAT-DTAPGAAGATAA 369
 Db 302 KWKKAVRVTTLMLKRLAPQSSST-AAAGASAT-DTAPGAAGATAA 358
 QY 370 AARAAKSDNVAPADRSATPATD 391
 Db 359 -----GSELPAPAPSSSRAMD 374

RESULT 4

S57347
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
 N/Alternate names: CamKI
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: S57347
 R/Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tomhave, E.D.; Edelman, A.M.;
 EMBO J. 14, 3679-3686, 1995
 A/Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain struct

A:Reference number: S57347, MUID:95369239, PMID:7641687
A:Accession: S57347
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-370 <HAR>
A:Cross-references: EMBL:U41816, NID:g790789, PIDN:AAA99458.1, PID:g790790
C:Genetics:
A:Gene: GDB:CAMK1
A:Cross-references: GDB:642249
C:Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransferase
F:18-276/Domain: protein kinase homology <KIN>
F:26-34/Region: protein kinase ATP-binding motif
F:293-299/Region: autophosphorylation
F:302-314/Region: calmodulin binding
F:177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 30.7%; Score 793; DB 1; Length 370;
Best Local Similarity 43.7%; Pred. No. 3.9e-27;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;

QY 14 YNCPSEVTVDRDLQGVITKEEFCEIFRAKDKTKGKLTCKKFEQKRDGRKVRKAQKNGIGI 73
DB 10 WKQHEPDRIDYDFRDVLTGAFSEVILAEDEKRTQKLVAKICIAKEALEGKESKEMENIAY 69
QY 74 LKQVXHNPIQLVDFVTRKREYFIFELATGREVFDMILDQGYYSERDTSNVVRQVLEAV 133
DB 70 LHKIKHNIVALDITYSGGHTYIMQVLVSGEFLPDIYERKFTYTERDASRLIFQVLIDAY 129
QY 134 AYHSLKIVHNLKLENLVYNNRLKNSKIVISDFHLAKLEN--GLIKEPGCTPEYLAPEV 191
DB 130 KYLHDLGIVARHDLKPNLNLVYSLDESKIMISDFGLKMEDEPGSVLSTAGCTGYVAPEV 189
QY 192 VGRQRYPVPDCAIGVIMYTLISGNPPFEVEVEDDYENHDKNLFKKIILAGDYEPDSPY 251
DB 190 LAQKPYKAVADQWISGIVAYITLLCGYPPFYDE-----NDALFQIILKAEYEPDSPY 241
QY 252 WDIISQAQKLVTRLMVEVDQRTTAEALSHWISGNAASDKNIKQVCAQIEKYNARA 311
DB 242 WDIISDAKQIFRLMEKDPKRFCTQALQHPFIADDTLADKNITHOSVEBQIKNFASKS 301
QY 312 KMKKAVVTTLMKRLRAPE--QSSTAAQSKATDTATPGAGATATAAASGATSAP 366
DB 302 KMKQAPNATVAVRMKRLQLGTSQEGGQRTASHBELTTPVAGGPAAGCCCRDCCVEP 358

RESULT 5

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - Caenorhabditis elegans
T37321
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text change 21-Jul-2000
C:Accession: T37321
R:Bio. Chem. 274, 22556-22562, 1999
J. Biol. Chem. 274, 22556-22562, 1999
A:Title: Ca2+/calmodulin-dependent protein kinase cascade in Caenorhabditis elegans. Top
A:Reference number: Z21686, MUID:99357789, PMID:10428833
A:Accession: T37321
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-348 <ETD>
A:Cross-references: EMBL:AB021864, NID:g5672677, PIDN:BA82674.1, PID:g5672678
A:Experimental source: strain Bristol N2; embryonic stage
C:Genetics:
A:Note: cmk-1
C:Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransferase

Query Match 27.6%; Score 713; DB 2; Length 348;
Best Local Similarity 43.1%; Pred. No. 8.8e-24;
Matches 137; Conservative 75; Mismatches 96; Indels 10; Gaps 3;

QY 20 VTDKRYDQGVITKEEFCEIFRAKDKT-TGKLTCKKQKRDGRKVRKAQKNGIILKMKV 78

DB 18 IREKIDPFDVLTGAFSKYFLAESKSDAGQMTAVKCIDKALKGKESLENEIKTLRKLR 77
QY 79 HENIQLVDFVTRKREYFIFELATGREVFDMILDQGYYSERDTSNVVRQVLEAVAYHLS 138
DB 78 HNNIVQLFDTYERQKQFVTLVWELVTGSELPDRIVAKGSYTERDQASNLIRQVLEAVGFVMD 137
QY 139 LKIVHNLKLENLVYNNRLKNSKIVISDFHLAKLE--NLIKEPGCTPEYLAPEVGRQRV 197
DB 138 NGVHVRHDLKPNLNLVYNNRLKNSKIVISDFHLAKLE--NLIKEPGCTPEYLAPEVGRQRV 197
QY 198 GSPVPCMAIGVIMYTLISGNPPFEVEVEDDYENHDKNLFKKIILAGDYEPDSPYMDISQ 257
DB 198 GRAVDWMSIGVAYITLLCGYPPFYDE-----SDANLFAQIILKAEYEPDQISG 249
QY 258 AAKDVLTRLMVEVDQRTTAEALSHWISGNAASDKNIKQVCAQIEKNFAPAKKAV 317
DB 250 SAKDPTIHMCCDPBARFTCODALSHPWISGNTATYTHIHGTVAHVLKSLAKRWKAY 309
QY 318 RYTTLMKRLRAPEQGSTA 335
DB 310 NAAAIAPQLQMLRLSSNS 327

RESULT 6

B88640
Protein K07A9.2 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence revision 10-May-2001 #text change 24-Aug-2001
C:Accession: B88640
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000, MUID:99069613, PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.ganger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: B88640
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <STO>
A:Cross-references: GB:chr_IV, PIDN:AAC68810.1, PID:g3790765, GSPDB:GN00022, CESP:K07A9.2
C:Genetics:
A:Gene: K07A9.2
A:Map position: 4
C:Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology

Query Match 25.0%; Score 645.5; DB 2; Length 310;
Best Local Similarity 46.0%; Pred. No. 5.6e-21;
Matches 125; Conservative 58; Mismatches 76; Indels 13; Gaps 3;

RESULT 7

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - rat
T37324
QY 69 NEEGLIKM-----VKPNILQLVDFVTRKREYFIFELATGREVFDMILDQGYYSERDTSN 124
DB 26 NEFKKEKEPIFLRNHNYQLFDYDEKQFVTLVWELVTGSELPDRIVAKGSYTERDQASN 85
QY 125 VVRQVLEAVAYHLSKIVHNLKLENLVYNNRLKNSKIVISDFHLAKLE--NLIKEPGCT 183
DB 86 LIRQVLEAVGFVMDNGVHVRHDLKPNLNLVYNNRLKNSKIVISDFHLAKLE--NLIKEPGCT 145
QY 184 PEYLAPEVGRQRYPVPDCAIGVIMYTLISGNPPFEVEVEDDYENHDKNLFKKIILAG 243
DB 146 PGYVAPEVLTQKPYGAVDWMSIGVAYITLLCGYPPFYDE-----SDANLFAQIILK 197
QY 244 DYEFDSPYMDISQAQKDVTRLMVEVDQRTTAEALSHWISGNAASDKNIKQVCAQ 303
DB 198 EYEFDAPIYWDQISDAKQFITIHMCCDPBARFTCODALSHPWISGNTATYTHIHGTVAH 257
QY 304 IENKPAKAKKAVVTTLMKRLRAPEQGSTA 335
DB 258 LKSLAKRWKAYNAAAIAPQLQMLRLSSNS 289

QY 336 AAGSASATDTATPGAGATPAAAGATSAPEGDAAPAKSDNV 379
 Db 373 IQESNRKASSAQPADQKDTXPLENMQGDHBAAPAADEMT 416

RESULT 9

A53036
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - human
 N:Alternate names: Ca2+/calmodulin-dependent protein kinase Gr; Cal-kinase IV
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: A53036; J02261; I53768
 R:Mosialos, G.; Hanislian, S.H.; Jawahar, S.; Vara, L.; Kieff, E.; Chatilla, T.A.
 J. Virol. 68, 1697-1705, 1994
 A:Title: A Ca(2+)/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed after tr
 A:Reference number: A53036; MUID:94149862; PMID:8107230
 A:Accession: A53036
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-473 <M60>
 A:Cross-references: GB:I24959; NID:g407005; PIDN:AAA18251.1; PID:g407006
 R:Kitani, T.; Okuno, S.; Fujisawa, H.
 J. Biochem. 115, 637-640, 1994
 A:Title: cDNA cloning and expression of human calmodulin-dependent protein kinase IV.
 A:Reference number: J02261; MUID:94375404; PMID:8089075
 A:Accession: J02261
 A:Molecule type: mRNA
 A:Residues: 1-473 <KIT>
 A:Cross-references: GB:P0742; NID:g487908; PIDN:BA06403.1; PID:g871845
 R:Blund, M.M.; Monroe, R.S.; Omstede, C.
 Gene 142, 191-197, 1994
 A:Title: The cDNA sequence and characterization of the Ca2+/calmodulin-dependent protein
 A:Reference number: I53768; MUID:94252566; PMID:8194751
 A:Accession: I53768
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-473 <RBS>
 A:Cross-references: GB:I17000; NID:g306478; PIDN:AAA35639.1; PID:g306479
 C:Comment: This protein is a Ca2+-responsive multifunctional protein kinase, which occur
 s system and in the immune system.
 C:Genetics:
 A:Gene: GDB:ILK
 A:Cross-references: GDB:6155815; OMIM:602366
 A:Map position: 11p15.5-11p15.4
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
 C:Keywords: ATP; calcium binding; calmodulin binding; phosphoprotein; phosphotransferase
 F:44-300/Domain: protein kinase homology <KIN>
 F:52-60/Region: protein kinase ATP-binding motif
 F:320-329/Region: calmodulin binding #status predicted
 F:8,12,15/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 23.6%; Score 608; DB 1; Length 473;
 Best Local Similarity 37.5%; Pred. No. 3.3e-19;
 Matches 141; Conservative 71; Mismatches 140; Indels 24; Gaps 6;

QY 38 IFPAKDKTGTGLTKCKFKQKGRKVRKAANKIGILMKVGNPILQVDFVTRKEYFI 97
 Db 60 VYRCQKQKQKPYALKVTKTVDKKI--VREIVGLRLSHPIIKKEIFETPTISL 116
 QY 98 FLEIATGREVFDMIDQGYISERDTSNVVRQVLEAVAYLHSKIVHRNKLKENTVYVNR 157
 Db 117 VLEIVTGGELFRIYVEKGYISERDADAVKQILEAVAYLHENGIVHRDLKPENLVYATPA 176
 QY 158 KNSKIVISDFHLAKL--ENGLIKPCCGPEYLAPEVNGRQYGRPVDCMAIGVIMYILLS 215
 Db 177 PDAPLKIAIDFGSKIVEHQVLMKTVCGTFGCAPEILRGCAVGEVDMWSGIIITYILLC 236
 QY 216 GNPPYEEVEEDDYENHDKNLFRKLIAGDYEFDSPYWMDISQAADIVYTRLMVEQDQRI 275
 Db 237 GPEPFD-----ERGDQPMFRRLINCEYFISPMWDEVSLNAKDLYVKLIIVDPKKRL 289

Db 290 TTFQALQHPWVTGKAAANFVEM-DTAAQKTLQEFNRRKLIKAIVKAVVASSRLGSASSSGS 348
 QY 336 AAGSASATDTATPGAGATPAAAGATPAAAGATSAPEGDAAPAKSDNVAPADR 384
 Db 349 IQESNRKASSAQPADQKDTXPLENMQGDHBAAPAADEMT 416
 QY 385 SATPATDGSATPATDG 400
 Db 409 NAEBAFKVVPKXVEDG 424

RESULT 10

S17656
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S17656; A29878; I49571
 R:Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikelia, J.M.
 FEBS Lett. 289, 105-109, 1991
 A:Title: cDNA sequence and differential expression of the mouse Ca(2+)/calmodulin-depende
 A:Reference number: S17656; MUID:91372388; PMID:1893997
 A:Accession: S17656
 A:Molecule type: mRNA
 A:Residues: 1-469 <JON>
 A:Cross-references: EMBL:X58995; NID:g50366; PIDN:CAA41741.1; PID:g50367
 R:Sikelia, J.M.; Hahn, W.E.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3038-3042, 1987
 A:Title: Screening an expression library with a ligand probe: isolation and sequence of
 A:Reference number: A29878; MUID:87204263; PMID:3033675
 A:Accession: A29878
 A:Molecule type: mRNA
 A:Residues: 315-469 <SIX>
 A:Cross-references: GB:M16206; NID:g200360; PIDN:AAA39933.1; PID:g387512
 R:Sikelia, J.M.; Law, M.L.; Kao, F.
 Genomics 4, 21-27, 1989
 A:Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent I
 A:Reference number: I49571; MUID:89122027; PMID:2536634
 A:Accession: I49571
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 250-277; 'CPGI', 281-301, 'T', 303-338, 'X', 340-469 <RES>
 A:Cross-references: GB:J03057; NID:g192366; PIDN:AAA37366.1; PID:g192367
 A:Experimental source: brain
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
 C:Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/thr
 F:40-296/Domain: protein kinase homology <KIN>
 F:48-56/Region: protein kinase ATP-binding motif
 F:306-469/Product: calpermin #status predicted <CSP>
 F:318-337/Region: calmodulin binding #status predicted
 F:71/Active site: lys #status predicted

Query Match 23.3%; Score 602.5; DB 1; Length 469;
 Best Local Similarity 34.1%; Pred. No. 5.6e-19;
 Matches 151; Conservative 75; Mismatches 180; Indels 37; Gaps 10;

QY 38 IFPAKDKTGTGLTKCKFKQKGRKVRKAANKIGILMKVGNPILQVDFVTRKEYFI 97
 Db 56 VYRCQKQKQKPYALKVTKTVDKKI--VREIVGLRLSHPIIKKEIFETPTISL 112
 QY 98 FLEIATGREVFDMIDQGYISERDTSNVVRQVLEAVAYLHSKIVHRNKLKENTVYVNR 157
 Db 113 VLEIVTGGELFRIYVEKGYISERDADAVKQILEAVAYLHENGIVHRDLKPENLVYATPA 172
 QY 158 KNSKIVISDFHLAKL--ENGLIKPCCGPEYLAPEVNGRQYGRPVDCMAIGVIMYILLS 215
 Db 173 PDAPLKIAIDFGSKIVEHQVLMKTVCGTFGCAPEILRGCAVGEVDMWSGIIITYILLC 232
 QY 216 GNPPYEEVEEDDYENHDKNLFRKLIAGDYEFDSPYWMDISQAADIVYTRLMVEQDQRI 275
 Db 233 GPEPFD-----ERGDQPMFRRLINCEYFISPMWDEVSLNAKDLYVKLIIVDPKKRL 285

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Db      286 TTFQALQHFWVTKANFVEM-DTAKKLOEFNARKKAAYKAVVASSRSGSASSSTS 344
Qy      336 AAQS--ASATDTATGAGAGATTAAGAAGATSAPEGDAAARA-AKSDNVAPADRSATPATDG 392
Db      345 IOENKASDPPSTQDAKSTDLGKKQGEDEEDQYEAASADBMKLO----- 395
Qy      393 SATPATDGSVTPATDGSITPATDGSVTPVTPDRSATPATDGRATPATDEESTVPTQSSAML 452
Db      396 SEVEEDKAGVKEEETSMWP-ODPEDELETDDPEMKRDESEKXKVEEEMPMTEBEA-- 452
Qy      453 ATKAAATPEPMAQP--DSTAPE 473
Db      453 -----PDAGLVPPQDAIQPE 468

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RESULT 11

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A45025
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999
C:Accession: A45025, S18915
R:Karis, U.; Muller, U.; Gilbert, D.J.; Copeland, N.G.; Jenkins, N.A.; Harbers, K.
Mol. Cell. Biol. 12, 3644-3652, 1992
A:Title: Structure, expression, and chromosome location of the gene for the beta subunit
of the lethal mouse mutant.
A:Reference number: A45025, MUID:92334366; PMID:1321343
A:Accession: A45025
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-542 <KAR>
A:Cross-references: GB:X63615; GB:S40077; NID:G50275; PIDN:CAA45160.1; PID:G50276
A:Experimental source: BALB/c brain
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:108750, NCBI:P108751)
R:Karis, U.; Mueller, U.; Gilbert, D.J.; Copeland, N.G.; Jenkins, N.A.; Harbers, K.
submitted to the EMBL Data Library, December 1991
A:Reference number: S18915
A:Accession: S18915
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-542 <KAR>
A:Cross-references: EMBL:X63615; NID:G50275; PIDN:CAA45160.1; PID:G50276
C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: acts on a variety of intracellular proteins; alpha and beta chains are expressed
C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase ATP-binding motif
F:287-311/Region: calmodulin binding #status predicted
F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

```

Query Match 21.4%; Score 552; DB 1; Length 542;

Best Local Similarity 32.7%; Pred. No. 8, 9e-17;

Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

21 TDRYDLOGVKTBEFCIFRAKDKTG-----KLHTCKKQKRGKVRKAANKELGIK 75

Db 11 TDEYQLVEEIGKAFSVRRVCVKLCTGHEHYAAKIINTKLSADHQLEBEAR-----ICR 66

Qy 76 MTKHPNLTQVDVVTTRKEFFILELATGREVDMILDOGYSESDTSNVVRQVLEAVAY 135

Db 67 LTKHSNIVRLHDSISEGPHYIVFDVTGELFEDIVARFYSEADASHCIQOILEAVLH 126

Qy 136 LHSIKIVRNKLENTLYVNRKNSKIVISDFHLAKLENGLIKE---PCGTPEYLAPEV 192

Db 127 CHQGVVHRDLKPEENLLASKKGAAYKLDLFGIALTEVQDDQAMFGAGTPEGLSPVIL 186

Qy 193 GRQRYGPRVDCMAIGVIMYLLSGNPFVEVEDVDENHDKLFFKILLAGVEFDSPPW 252

```

Db      187 RKEAYGPVDIMACGIVILYLVNGVPPFWE-----DQH--KLVOQIKAGADYFSPK 238
Qy      253 DDISQAADLVTRIMEVEVDQRTAEBAISHEMI--SGNAADKNTKDGV-CAQIEKNPA 309
Db      239 DVTPEAKNLINQMLTINPAKRITAEHALKHPVQCQSTVASMHRQETVEC--LKKFNA 296
Qy      310 RAKKKAIVRTYITMLKRLAPESGSTAAQASATDTATGAGAGATTAAGAAGATSAPEGD 369
Db      297 RRLKKGALITTMATATNFSVGRQTAPATWST-----ASGTTGVLVEQKSLN-- 346
Qy      370 AABAASDNVAPADRSATPATDGSATPATDGSVTPA-----TDGSITPATDGS 417
Db      347 ----KADGVKFPQTN--TKNSAATSPKGSJPPALAEQTTVINPVDG-IKESDST 358
Qy      418 VTPVTPDRSATPATDGRATPATDEESTVPTQ 447
Db      399 NTIIEDEA-----KARKQEIITTE 419

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RESULT 12

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A26464
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 11-Jun-1999
C:Accession: A26464
R:Bennett, M.K.; Kennedy, M.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1794-1798, 1987
A:Title: Deduced primary structure of the beta-subunit of brain type II Ca(2+)-calmodulin
A:Reference number: A26464, MUID:87175563; PMID:3470758
A:Accession: A26464
A:Molecule type: mRNA
A:Residues: 1-542 <BEN>
A:Cross-references: GB:M16112; NID:G206170; PIDN:AAA1866.1; PID:G206171
C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: acts on a variety of intracellular proteins; alpha and beta chains are expressed
C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase ATP-binding motif
F:287-311/Region: calmodulin binding #status predicted
F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

```

Query Match 21.3%; Score 551; DB 1; Length 542;

Best Local Similarity 32.7%; Pred. No. 9, 8e-17;

Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

21 TDRYDLOGVKTBEFCIFRAKDKTG-----KLHTCKKQKRGKVRKAANKELGIK 75

Db 11 TDEYQLVEEIGKAFSVRRVCVKLCTGHEHYAAKIINTKLSADHQLEBEAR-----ICR 66

Qy 76 MTKHPNLTQVDVVTTRKEFFILELATGREVDMILDOGYSESDTSNVVRQVLEAVAY 135

Db 67 LTKHSNIVRLHDSISEGPHYIVFDVTGELFEDIVARFYSEADASHCIQOILEAVLH 126

Qy 136 LHSIKIVRNKLENTLYVNRKNSKIVISDFHLAKLENGLIKE---PCGTPEYLAPEV 192

Db 127 CHQGVVHRDLKPEENLLASKKGAAYKLDLFGIALTEVQDDQAMFGAGTPEGLSPVIL 186

Qy 193 GRQRYGPRVDCMAIGVIMYLLSGNPFVEVEDVDENHDKLFFKILLAGVEFDSPPW 252

Db 187 RKEAYGPVDIMACGIVILYLVNGVPPFWE-----DQH--KLVOQIKAGADYFSPK 238

Qy 253 DDISQAADLVTRIMEVEVDQRTAEBAISHEMI--SGNAADKNTKDGV-CAQIEKNPA 309

Db 239 DVTPEAKNLINQMLTINPAKRITAEHALKHPVQCQSTVASMHRQETVEC--LKKFNA 296

Qy 310 RAKKKAIVRTYITMLKRLAPESGSTAAQASATDTATGAGAGATTAAGAAGATSAPEGD 369

Db 297 RRLKKGALITTMATATNFSVGRQTAPATWST-----ASGTTGVLVEQKSLN-- 346

QY 370 AARAKSDNVAPADRSATPATDGSATPATDGSVTPA-----TDGSINPATDGS 417
Db 347 ---KKADGVAFQINS---TKSSAITSFKGSLPALPEQTVIHNPPVG-IKSSDST 398
QY 418 VTPVDSRATPATDGRATPATDGSVTPPTQ 447
Db 399 NTIEDDA-----KARKQRIKITE 419

RESULT 13

568470
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta-3 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Jun-1999
C/Accession: S68470; 153501
R/Urguidi, V.; Ashcroft, S.J.H.
FEBS Lett. 358, 23-26, 1995
A/Title: A novel pancreatic beta-cell isoform of calcium/calmodulin-dependent protein ki
A/Reference number: 153501; MUID:95121451; PMID:7821422
A/Accession: S68470
A/Molecule type: mRNA
A/Residues: 1-589 <UNQ>
A/Cross-references: EMBL:X83375; NID:603580; PIDN:CAA58289.1; PID:603581
A/Experimental source: pancreatic islets
C/Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
C/Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C/Keywords: alternative splicing; ATP; autophosphorylation; calmodulin binding; phospho
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase ATP-binding motif
F:287-311/Region: calmodulin binding #status predicted
F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query March 21.1%; Score 545.5; DB 2; Length 589;
Best Local Similarity 30.4%; Pred. No. 1.8e-16;
Matches 143; Conservative 96; Mismatches 173; Indels 59; Gaps 13;
QY 21 TDRYDLGVITKEEFCIFRAKDKTTG-----KLHTCKFKQGRDKRYKAKKEIGLK 75
Db 11 TDEQVLVDIGKAFSVRRVCYKCTGHEVYAKIINTKLSARHQKLERAR---ICR 66
QY 76 MYKHPNIIQLVDVFTVTRKEFFILELATGREVFPMILDQGYSEBDSNVVRQVLEAVAY 135
Db 67 LKGSNIIVRLHDSISEEGFHYLVFDLVGGLFEDIVAREYSEADASHCIQQLLEAVH 126
QY 136 LHSKTIYHNLKLENLVYVNRKSKIVISDFHLAKENGLIKE---PGTPEYLAPEV 192
Db 127 CHQGVVVRHDLKPEHLILASCKCKGAIVKLADFGLAIEVGQDQAMFGPAGTGYLSBEVL 186
QY 193 GRQVGRVDDCAVGMVIMYIILSGNPPFEVEEDVDENHDKLFRKILAGDYFEDSPY 252
Db 187 RKEAYGRVVDIWACGVILYILVGYPPFWDE-----DQH--KLVOQIKGAVDYFSPBW 238
QY 253 DDISOAKDLVTRIMEVEDODRITAEBAISHEMI--SGNAASDKINIDGV-CAQIEKNFA 309
Db 239 DTVPEAKNLINQMLTINPAKRIITHKIPWICQGSSTVASMHRQETVEC--LKKFNA 296
QY 310 RAKMKKAVRVTTLMKRLAPESOS-----STAAQASATDTATPAGAGATPAA 358
Db 297 RRLKGAIIITMLTRNFSAKSLINKKADGVKPTQNSTKSSAI--TSPKSLPALAES 355
QY 359 ASGATSAEAGAAAKSDNVAPADR--SATPATDGSATPATDGSVTPATDGSIT--TPA 413
Db 356 SDSTVTTIEDDAKAPRISIDINSVRRQGTPEAEGPSVGPAPCLPGLGIPPTSPSR 415
QY 414 TDGSAVTPDTSATPATDGS-----RATPATDGSVTPPTQ 447
Db 416 ISDINSVRRSGTPEAEGLPVGPFPQPSPTLPGLPTFPRKQEIITKITE 466

RESULT 14

A31908
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma-a chain - rat

C/Species: Rattus norvegicus (Norway rat)
C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 11-Jun-1999
C/Accession: A31908
R/Tobimatsu, T.; Kameshita, I.; Fujisawa, H.
J. Biol. Chem. 263, 16082-16086, 1988
A/Title: Molecular cloning of the cDNA encoding the third polypeptide (gamma) of brain c
A/Reference number: A31908; MUID:89034067; PMID:2846534
A/Accession: A31908
A/Molecule type: mRNA
A/Residues: 1-527 <TOR>
A/Cross-references: GB:J04063; NID:9206151; PIDN:AAA1857.1; PID:9206152
C/Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
C/Function: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Note: acts on a variety of intracellular proteins; gamma and delta chains are expressec
C/Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C/Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase ATP-binding motif
F:287-311/Region: calmodulin binding #status predicted
F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query March 21.0%; Score 542; DB 1; Length 527;
Best Local Similarity 34.4%; Pred. No. 2.3e-16;
Matches 141; Conservative 77; Mismatches 146; Indels 46; Gaps 13;

QY 21 TDRYDLGVITKEEFCIFRAKDKTT-----GKHTCKFKQGRDKRYKAKKEIGLK 75
Db 11 TDDQVLFEELGKAGSVARRCYKKTSTGEYAKIINTKLSARHQKLERAR---ICR 66
QY 76 MYKHPNIIQLVDVFTVTRKEFFILELATGREVFPMILDQGYSEBDSNVVRQVLEAVAY 135
Db 67 LKHPNIVLHDSISEEGFHYLVFDLVGGLFEDIVAREYSEADASHCIQQLLESVNH 126
QY 136 LHSKTIYHNLKLENLVYVNRKSKIVISDFHLAKENGLIKEP-----CGTPEYLAPE 189
Db 127 IQHNDIVHDLKPEHLILASCKCKGAIVKLADFGLAIEVGQDQAMFGPAGTGYLSBP 183
QY 190 EYVGRGRVPRVDCAVGMVIMYIILSGNPPFEVEEDVDENHDKLFRKILAGDYFEDSP 249
Db 184 EYLRKDPYKRPVDIYACGIIYILVGYPPFWDE-----DQH--KLVOQIKGAVDYFSP 235
QY 250 PWDIDISQAKDLVTRIMEVEDODRITAEBAISHEMI--SGNAASDKINIDGV-CAQIEK 306
Db 236 FEMDTITPAKLNINQMLTINPAKRIITHDALKHFWCQGSSTVASMHRQETVEC--LRK 293
QY 307 NFAPAKKAVRVTTLMKRLAPESOSTTAAQASATDTATPAGAGATPAAAGATSA 365
Db 294 FNAARLTKAIIITMLVSNFSVGRQSSAPAPAS-----AAGLAGQAKSLINKK 345
QY 366 PEGDAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATD 415
Db 346 SDGVKKRKSSTSVHIMEPQTVVHN-----ATDQ-IKGSTSCNTTIED 389

RESULT 15

UC5636
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma-E - human
C/Species: Homo sapiens (man)
C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 17-Mar-1999
C/Accession: UC5636
C/Breen, M.A.; Ashcroft, S.J.H.
Biochem. Biophys. Res. Commun. 226, 473-478, 1997
A/Title: Human islets of Langerhans express multiple isoforms of calcium/calmodulin-deper
A/Reference number: UC5636; MUID:97282459; PMID:9240463
A/Accession: UC5636
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-556 <BRE>
A/Cross-references: GB:U66063
C/Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C/Keywords: phosphotransferase

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:45:29 ; Search time 45 Seconds

(without alignments)
3512.769 Million cell updates/sec

Title: US-10-669-689-2

Perfect score: 2581 1 MFGCVTLGDKKXKNYQPSRV.....SSKGEAAGYAQDSQREAS 501

Sequence: 1 MFGCVTLGDKKXKNYQPSRV.....SSKGEAAGYAQDSQREAS 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MNC:*
8: SP_ORGANELLE:*
9: SP_PLANT:*
10: SP_TODENT:*
11: SP_VIRUS:*
12: SP_YEAST:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2577	99.8	501	4 Q8WTT8	Q8WTT8 homo sapien
2	2568	99.5	501	4 Q8WTT8	Q8WTT8 homo sapien
3	2563	99.3	501	4 Q8WTT8	Q8WTT8 homo sapien
4	2410.5	93.4	512	11 Q8WTT8	Q8WTT8 mus musculu
5	2403	93.1	473	4 Q8WTT8	Q8WTT8 mus musculu
6	2402.5	93.1	473	4 Q8WTT8	Q8WTT8 mus musculu
7	2398.5	92.9	470	4 Q8WTT8	Q8WTT8 mus musculu
8	2383.5	92.3	504	11 Q8WTT8	Q8WTT8 mus musculu
9	2383.5	92.3	504	11 Q8WTT8	Q8WTT8 mus musculu
10	1602	62.1	333	4 Q8WTT8	Q8WTT8 mus musculu
11	1537.5	59.6	421	13 Q8WTT8	Q8WTT8 mus musculu
12	786.5	30.5	13	Q8WTT8	Q8WTT8 mus musculu
13	771	29.9	357	4 Q8WTT8	Q8WTT8 mus musculu
14	767.5	29.7	385	4 Q8WTT8	Q8WTT8 mus musculu
15	767.5	29.7	385	4 Q8WTT8	Q8WTT8 mus musculu
16	764.5	29.6	367	11 Q8WTT8	Q8WTT8 mus musculu

17	762	29.5	378	13 Q8WTT8	Q8WTT8 mus musculu
18	761	29.5	377	13 Q8WTT8	Q8WTT8 mus musculu
19	757.5	29.3	382	11 Q8WTT8	Q8WTT8 mus musculu
20	749	29.0	476	11 Q8WTT8	Q8WTT8 mus musculu
21	748.5	29.0	405	5 Q8WTT8	Q8WTT8 mus musculu
22	747.5	29.0	481	4 Q8WTT8	Q8WTT8 mus musculu
23	746.5	28.9	476	4 Q8WTT8	Q8WTT8 mus musculu
24	746	28.9	460	4 Q8WTT8	Q8WTT8 mus musculu
25	743.5	28.8	477	11 Q8WTT8	Q8WTT8 mus musculu
26	743.5	28.8	477	11 Q8WTT8	Q8WTT8 mus musculu
27	731	28.3	299	11 Q8WTT8	Q8WTT8 mus musculu
28	720	27.9	309	11 Q8WTT8	Q8WTT8 mus musculu
29	716.5	27.8	342	11 Q8WTT8	Q8WTT8 mus musculu
30	716	27.7	377	11 Q8WTT8	Q8WTT8 mus musculu
31	715	27.7	343	11 Q8WTT8	Q8WTT8 mus musculu
32	715	27.7	343	11 Q8WTT8	Q8WTT8 mus musculu
33	715	27.7	348	5 Q8WTT8	Q8WTT8 mus musculu
34	715	27.7	355	11 Q8WTT8	Q8WTT8 mus musculu
35	713	27.6	348	5 Q8WTT8	Q8WTT8 mus musculu
36	705.5	27.3	324	5 Q8WTT8	Q8WTT8 mus musculu
37	660.5	25.6	284	5 Q8WTT8	Q8WTT8 mus musculu
38	659.5	25.6	284	5 Q8WTT8	Q8WTT8 mus musculu
39	620.5	24.0	502	11 Q8WTT8	Q8WTT8 mus musculu
40	604.5	23.4	469	11 Q8WTT8	Q8WTT8 mus musculu
41	589	22.8	385	13 Q8WTT8	Q8WTT8 mus musculu
42	578.5	22.4	716	4 Q8WTT8	Q8WTT8 mus musculu
43	577.5	22.4	424	11 Q8WTT8	Q8WTT8 mus musculu
44	575	22.3	755	11 Q8WTT8	Q8WTT8 mus musculu
45	563.5	21.8	695	4 Q8WTT8	Q8WTT8 mus musculu

ALIGNMENTS

RESULT 1
ID Q8WTT8 PRELIMINARY; PRT; 501 AA.
AC Q8WTT8;
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strausberg R.;
RL Submitted (DBE-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019256; AA017363.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 501 AA; 54353 MW; 1D6BFAADID70 CRC64;

Query Match 99.8%; Score 2577; DB 4; Length 501;
Best Local Similarity 99.8%; Pred. No. 8.5e-147;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MFGCVTLGDKKXKNYQPSRVTDRLDGVTKTEEFCEIFRAKDTGKLTGKPKFQKRG 60
1 MFGCVTLGDKKXKNYQPSRVTDRLDGVTKTEEFCEIFRAKDTGKLTGKPKFQKRG 60

Query Match 99.3%; Score 2563; DB 4; Length 501;
Best Local Similarity 99.6%; Pred. No. 5,9e-146;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 MPEGCVTLDGKKNNQPSSEVTDRLDGVITKEEFCIFPAKDKTTGKLATCKKFKQKDG 60
D 1 MPEGCVTLDGKKNNQPSSEVTDRLDGVITKEEFCIFPAKDKTTGKLATCKKFKQKDG 60
QY 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVPMIILQGYSER 120
D 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVPMIILQGYSER 120
QY 121 DTSNVVRQYLEAVAYLHSLKIVHRNLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
D 121 DTSNVVRQYLEAVAYLHSLKIVHRNLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
QY 181 CGTPEYLAPEVVGQRGRPYDCAIGVIMYILSGNPPFEEVEEDDYENHDKLFRKI 240
D 181 CGTPEYLAPEVVGQRGRPYDCAIGVIMYILSGNPPFEEVEEDDYENHDKLFRKI 240
QY 241 LAGDYEPDSPYWDISQAAXDLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
D 241 LAGDYEPDSPYWDISQAAXDLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
QY 301 CAQIEKNFAPAKKKAIVTTLMKRLAPBEGSSTAASADTATPGAAAGATAAAS 360
D 301 CAQIEKNFAPAKKKAIVTTLMKRLAPBEGSSTAASADTATPGAAAGATAAAS 360
QY 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
D 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
QY 421 VTDRSATPATDGRATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 480
D 421 VTDRSATPATDGRATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 480
QY 481 PSSKGEBAAGYAQESQREBAS 501
D 481 PSSKGEBAAGYAQESQREBAS 501
```

RESULT 4

Q8VD20 PRELIMINARY; PRT; 512 AA.

AC Q8VD20; PRELIMINARY; PRT; 512 AA.
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to vesicle-associated calmodulin-binding protein.
GN BC017634.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017634; AA017634.1; -.
DR MGD; MGI:2384296; BC017634.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002290; Ser Thr_kinase.
DR Pfam; PF00069; Pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; transferase.

SQ SEQUENCE 512 AA; 54819 MW; CFEFD4C43CC869A9 CRC64;

Query Match 93.4%; Score 2410.5; DB 11; Length 512;
Best Local Similarity 92.2%; Pred. No. 8.6e-137;
Matches 474; Conservative 6; Mismatches 19; Indels 15; Gaps 2;

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QY 1 MPEGCVTLDGKKNNQPSSEVTDRLDGVITKEEFCIFPAKDKTTGKLATCKKFKQKDG 60
D 1 MPEGCVTLDGKKNNQPSSEVTDRLDGVITKEEFCIFPAKDKTTGKLATCKKFKQKDG 60
QY 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVPMIILQGYSER 120
D 61 RKVRAAKNEIGILKXVHPNIIQLVDVFTVRKEYFIFLELATGREVPMIILQGYSER 120
QY 121 DTSNVVRQYLEAVAYLHSLKIVHRNLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
D 121 DTSNVVRQYLEAVAYLHSLKIVHRNLKLENLVYNRKNSKIVISDFHLAKLENGLKEP 180
QY 181 CGTPEYLAPEVVGQRGRPYDCAIGVIMYILSGNPPFEEVEEDDYENHDKLFRKI 240
D 181 CGTPEYLAPEVVGQRGRPYDCAIGVIMYILSGNPPFEEVEEDDYENHDKLFRKI 240
QY 241 LAGDYEPDSPYWDISQAAXDLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
D 241 LAGDYEPDSPYWDISQAAXDLVTRLMEVEODQRTAEBAISHWISGNAASDKNIKXGV 300
QY 301 CAQIEKNFAPAKKKAIVTTLMKRLAPBEGSSTAASADTATPGAAAGATAAAS 359
D 301 CAQIEKNFAPAKKKAIVTTLMKRLAPBEGSSTAASADTATPGAAAGATAAAS 358
QY 360 -----SGATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATD 407
D 360 -----SGATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATD 407
QY 408 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 467
D 408 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 467
QY 419 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 478
D 419 GSITPATDGSVTPVDRSATPATBESVPTTQSSAMLATKAATPEPMAQDSTAPGATGQAP 478
QY 468 DSTAPEGATGQAPSSKGEBAAGYAQESQREBAS 501
D 468 DSTAPEGATGQAPSSKGEBAAGYAQESQREBAS 501
D 479 DSTALEGATGQAPSSKGEBAAGYAQESQREBAS 512
```

RESULT 5

Q9H005 PRELIMINARY; PRT; 473 AA.

AC Q9H005; PRELIMINARY; PRT; 473 AA.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
DE DKFZP564E0482.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21154917; PubMed=11230166;
RX Wieman S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Anserge W., Boecker M., Bloeker H., Bauersachs S., Blum N.,
RA Lauber J., Duesterhoef A., Beyer A., Koehler K., Strack N.,
RA Mews H.W., Ottenwaelder B., Obermaier B., Tange J., Heubner D.,
RA Wambute R., Korn B., Klein W., Poustka A.;
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs";
RL Genome Res. 11:422-435(2001).
DR EMBL; AL13697; CAB6632.1; -.
DR HSSP; O63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

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DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00069; kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR Hypothetical protein: ATP-binding; Transferase.
SQ SEQUENCE 473 AA; 51208 MW; 8DFCE6C4F43262 CRC64;

Query Match 93.1%; Score 2403; DB 4; Length 473;
Best Local Similarity 94.2%; Pred. No. 2.2e-136;
Matches 472; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MPFGCVTLGDKKNYNPSEVTDRIYDVGQVKTBEFCEIFRAKDTGKLTCKKFKQRDG 60
DB 1 MPFGCVTLGDKKNYNPSEVTDRIYDVGQVKTBEFCEIFRAKDTGKLTCKKFKQRDG 60
QY 61 RKYRKAANEIGILKWKHPNIIQLVDVFTREKEYFIFELATGREVFDWILDQGYSER 120
DB 61 RKYRKAANEIGILKWKHPNIIQLVDVFTREKEYFIFELATGREVFDWILDQGYSER 120
QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
QY 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
DB 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
QY 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
DB 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
QY 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 300
DB 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 300
QY 213 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 272
DB 213 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 272
QY 301 CAQIEKNFAAKWKAVRVTTLMKRLAPESQSTAAQASATDTATPGAAGATPAAS 360
DB 273 CAQIEKNFAAKWKAVRVTTLMKRLAPESQSTAAQASATDTATPGAAGATPAAS 332
QY 361 GATSAPEGDAARAASDVAADRSATPATDGSATPATDGSITPATDGSVTP 420
DB 361 GATSAPEGDAARAASDVAADRSATPATDGSATPATDGSITPATDGSVTP 392
QY 333 GATSAPEGDAARAASDVAADRSATPATDGSATPATDGSITPATDGSVTP 392
DB 333 GATSAPEGDAARAASDVAADRSATPATDGSATPATDGSITPATDGSVTP 392
QY 421 VTDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 480
DB 393 ATDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 452
QY 481 PSSKGEAAGYAQESQREAS 501
DB 453 PSSKGEAAGYAQESQREAS 473

RESULT 6

Q8NC85 PRELIMINARY; PRT; 470 AA.
AC Q8NC85;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90418.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N. A.
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hito Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nishimura Y.,
RT "NEDO human cDNA sequencing project";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074899; BAC11278.1; -
DR GO:0005524; F:ATP binding; IEA

DR GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO:0016740; F:transferase activity; IEA.
DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR Hypothetical protein: ATP-binding; Transferase.
SQ SEQUENCE 470 AA; 51686 MW; 16CC94CED91EB893 CRC64;

Query Match 93.1%; Score 2402.5; DB 4; Length 470;
Best Local Similarity 93.6%; Pred. No. 2.3e-136;
Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

QY 1 MPFGCVTLGDKKNYNPSEVTDRIYDVGQVKTBEFCEIFRAKDTGKLTCKKFKQRDG 60
DB 1 MPFGCVTLGDKKNYNPSEVTDRIYDVGQVKTBEFCEIFRAKDTGKLTCKKFKQRDG 60
QY 61 RKYRKAANEIGILKWKHPNIIQLVDVFTREKEYFIFELATGREVFDWILDQGYSER 120
DB 61 RKYRKAANEIGILKWKHPNIIQLVDVFTREKEYFIFELATGREVFDWILDQGYSER 120
QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
QY 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
DB 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
QY 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
DB 121 DTSNVVRQVLEAVAYHSLKIVHRNKLLENLYYNNRLKNSKIYISDFHLAKLENGLIKEP 180
QY 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
DB 181 CGPEYLAPEVVGQRGRVPCDCAIGVIMTILSGNPPFYEEVEDDYENHDKNLFKRI 240
QY 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 300
DB 241 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 300
QY 213 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 272
DB 213 LAGDYFDSPYWDDISQAADLVTRIMEVEQDRIYAEASISHEWISGNAASDKNIKGV 272
QY 301 CAQIEKNFAAKWKAVRVTTLMKRLAPESQSTAAQASATDTATPGAAGATPAAS 360
DB 301 CAQIEKNFAAKWKAVRVTTLMKRLAPESQSTAAQASATDTATPGAAGATPAAS 350
QY 361 GATSAPEGDAARAASDVAADRSATPATDGSATPATDGSITPATDGSVTP 420
DB 361 GATSAPEGDAARAASDVAADRSATPATDGSATPATDGSITPATDGSVTP 389
QY 351 -----AARSATPATDGSATPATDGSITPATDGSITPATDGSVTP 389
DB 351 -----AARSATPATDGSATPATDGSITPATDGSITPATDGSVTP 389
QY 421 VTDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 480
DB 390 ATDRSATPATDGSATPATDGSITPATDGSITPATDGSITPATDGSVTP 449
QY 481 PSSKGEAAGYAQESQREAS 501
DB 450 PSSKGEAAGYAQESQREAS 470

RESULT 7

Q8NB58 PRELIMINARY; PRT; 470 AA.
AC Q8NB58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90813.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N. A.
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hito Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project";
 DR EMBL; AK075294; to the EMBL/GenBank/DBJ databases.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrcKc; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Hypothetical protein; ATP-binding; Transferase.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 470 AA; 51658 MW; 795A18DD242F082F CRC64;

Query Match 92.9%; Score 2398.5; DB 4; Length 470;
 Best Local Similarity 93.4%; Pred. No. 4.1e-136;
 Matches 468; Conservative 1; Mismatches 1; Indels 31; Gaps 1;

1 MPFGCVTLGDKKNVNPSEVTDRLDGVITKEEFCIFPAKDTGKLTCKKFKQKDG 60
 1 MPFGCVTLGDKKNVNPSEVTDRLDGVITKEEFCIFPAKDTGKLTCKKFKQKDG 60
 61 RYRKAANKNEIGILKMWGHPNIIQLVDVFTVTRKEYFIFLELATGREVDMILDOGYSER 120
 61 RYRKAANKNEIGILKMWGHPNIIQLVDVFTVTRKEYFIFLELATGREVDMILDOGYSER 120
 121 DTSNVVRQVLEAVAYLHSLKIYHRNLKLENLVYNNRKNKSKIYISDFHLAKLNLKEP 180
 121 DTSNVVRQVLEAVAYLHSLKIYHRNLKLENLVYNNRKNKSKIYISDFHLAKLNLKEP 180
 121 CGPEYLAPEVVGQRGRPVDCWALGVIMYLLSGNPPFYEEVEDDYENHDKLFRKI 240
 181 CGPEYLAPEVVGQRGRPVDCWALGVIMYLLSGNPPFYEEVEDDYENHDKLFRKI 240
 181 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 241 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 241 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 241 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 301 CAQIEKNFAPAKWKAVRVTTLMKRLAPESGSTAAASATPTATPAAAGATAAAS 360
 301 CAQIEKNFAPAKWKAVRVTTLMKRLAPESGSTAAASATPTATPAAAGATAAAS 360
 301 CAQIEKNFAPAKWKAVRVTTLMKRLAPESGSTAAASATPTATPAAAGATAAAS 360
 361 GATGAPEDDARAASDNVAPADRSATPATDGSATPATDGSATPATDGSATPATDGSATP 420
 361 GATGAPEDDARAASDNVAPADRSATPATDGSATPATDGSATPATDGSATPATDGSATP 420
 351 -----ADRSATPATDGSATPATDGSATPATDGSATPATDGSATPATDGSATP 389
 421 VTDRSATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRAT 480
 421 VTDRSATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRAT 480
 390 ATDGSATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRAT 449
 481 PSSKGEAAGYAQESQREAS 501
 450 PSSKGEAAGYAQESQREAS 470

RESULT 8
 063092 PRELIMINARY; PRT; 504 AA.
 AC 063092;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calmodulin-binding protein.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxId=10116;

RM [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=94110847; PubMed=8283228;
 RA Godbout M., Exlander M.G., Haseel K.W., Danielson P.E., Wong K.R.,
 RA Battemberg B.L., Foye P.E., Bloom F.E., Sutcliffe J.G.;
 RT "13S: a calmodulin-binding, vesicle-associated, protein kinase-like
 protein enriched in forebrain neurites";
 RL J. Neurosci. 14:1-13(1994).
 DR EMBL; L22557; AAA16533.1; -
 DR PIR; I56542; I56542.
 DR HSP; 063450; 1A06.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 504 AA; 54105 MW; DF31B414B213B54E CRC64;

Query Match 92.3%; Score 2383.5; DB 11; Length 504;
 Best Local Similarity 91.9%; Pred. No. 3.5e-135;
 Matches 468; Conservative 5; Mismatches 23; Indels 13; Gaps 2;

1 MPFGCVTLGDKKNVNPSEVTDRLDGVITKEEFCIFPAKDTGKLTCKKFKQKDG 60
 1 MPFGCVTLGDKKNVNPSEVTDRLDGVITKEEFCIFPAKDTGKLTCKKFKQKDG 60
 61 RYRKAANKNEIGILKMWGHPNIIQLVDVFTVTRKEYFIFLELATGREVDMILDOGYSER 120
 61 RYRKAANKNEIGILKMWGHPNIIQLVDVFTVTRKEYFIFLELATGREVDMILDOGYSER 120
 121 DTSNVVRQVLEAVAYLHSLKIYHRNLKLENLVYNNRKNKSKIYISDFHLAKLNLKEP 180
 121 DTSNVVRQVLEAVAYLHSLKIYHRNLKLENLVYNNRKNKSKIYISDFHLAKLNLKEP 180
 121 CGPEYLAPEVVGQRGRPVDCWALGVIMYLLSGNPPFYEEVEDDYENHDKLFRKI 240
 181 CGPEYLAPEVVGQRGRPVDCWALGVIMYLLSGNPPFYEEVEDDYENHDKLFRKI 240
 181 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 241 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 241 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 241 LAGDYFDPSPYWDNISQAADLVTRLMEVEODQRTAEALSHEMIISGNAASDKNIKGV 300
 301 CAQIEKNFAPAKWKAVRVTTLMKRLAPESGSTAAASATPTATPAAAGATAAAS 360
 301 CAQIEKNFAPAKWKAVRVTTLMKRLAPESGSTAAASATPTATPAAAGATAAAS 360
 301 CAQIEKNFAPAKWKAVRVTTLMKRLAPESGSTAAASATPTATPAAAGATAAAS 360
 361 G-----ATGAPEDDARAASDNVAPADRSATPATDGSATPATDGSATPATDGSATP 412
 361 G-----ATGAPEDDARAASDNVAPADRSATPATDGSATPATDGSATPATDGSATP 412
 356 GAAPAGSAGATGTGDDACCAKSDMASADRSATPATDGSATPATDGSATPATDGSATP 415
 413 ATDGSATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRAT 472
 413 ATDGSATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRAT 472
 416 ATDGSATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRATPATDGRAT 475
 473 EGATGQAPPSSKGEAAGYAQESQREAS 501
 476 EGATGQAPPSSKGEAAGYAQESQREAS 504

RESULT 9
 075749 PRELIMINARY; PRT; 436 AA.
 AC 075749;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Body;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Straussberg R.U., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinova K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileon M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney U., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Body;
 RA Straussberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC055127; AAH56127.1;
 KW Hypothetical protein.
 SQ SEQUENCE 436 AA; 48704 MW; ECC8209E29483EE CRC64;

Query Match 63.3%; Score 1635; DB 13; Length 436;
 Best Local Similarity 65.2%; Pred. No. 2,5e-90;
 Matches 320; Conservative 52; Mismatches 63; Indels 56; Gaps 7;

QY 1 MFGCVTTGDKKNYNQPSFVTDYDLGVYKTEBCEIFRAXDKTTGKLTCKKFKRKG 60
 DB 1 MFGCGLKPEKDYNSPFEITDKYDLGVYKSEEECFRAXDKTTKLTCKKFLKKG 60
 QY 61 RYRRAAKKEIILMKVHKNILQVDFVTRKEVFIFLELATGREGVDMILDOGYSER 120
 DB 61 RYRRAAKKEIILMKVHKNILQVDFVTRKEVFIFLELATGREGVDMILDOGYSER 120
 QY 121 DTSNVROYLVAAYLHSLKTVHRLKLENLYYVRLKNSKIVIDFHLAKLENGLIEP 180
 DB 121 DTSNVROYLVAAYLHSLKTVHRLKLENLYYVRLKNSKIVIDFHLAKLENGLIEP 180
 QY 121 DTSNVROYLVAAYLHSLKTVHRLKLENLYYVRLKNSKIVIDFHLAKLENGLIEP 180
 DB 121 DTSNVROYLVAAYLHSLKTVHRLKLENLYYVRLKNSKIVIDFHLAKLENGLIEP 180
 QY 181 CGTPEYLADEVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKI 240
 DB 181 CGTPEYLADEVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKI 240
 QY 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGV 300
 DB 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGV 300
 QY 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGV 300
 DB 241 LAGDYEFDPYDDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGV 300
 QY 301 CAQIEKNFAKWKKAIVTTLMKRLRAPEQSTAAQASATDTATGAAGATAAAS 360
 DB 301 CAQIEKNFAKWKKAIVTTLMKRLRAPEQSTAAQASATDTATGAAGATAAAS 360
 QY 361 GATSAPEGDAAPAKSDNVADPDRSATPATDGSATPATDGSVTPATDGSVTP 420
 DB 361 GATSAPEGDAAPAKSDNVADPDRSATPATDGSATPATDGSVTPATDGSVTP 420
 QY 337 ---TAAAEAAASPE-----ADPAAGQETGCA-----ASEASTAPSS----- 373
 DB 337 ---TAAAEAAASPE-----ADPAAGQETGCA-----ASEASTAPSS----- 373
 QY 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSATPEG-ATGCA 479
 DB 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSATPEG-ATGCA 479

DB 374 -TAEISIASIE---VPAVE-----PAAAEASAAVOPPAEPVTHVEPEEQVFTSRNGEA 425
 QY 480 PFSSKGEAEAG 490
 DB 426 PALDTVEQSG 436

RESULT 10
 Q8NDU4 PRELIMINARY; PRT; 333 AA.
 ID Q8NDU4
 AC Q8NDU4;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN DKFZ564G2082.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.,
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL833943; CAD38798.1;
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 333 AA; 34642 MW; 599E9307FF7D91E6 CRC64;

Query Match 62.1%; Score 1602; DB 4; Length 333;
 Best Local Similarity 99.1%; Pred. No. 1.7e-88;
 Matches 313; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 186 YLAPYVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKIAGY 245
 DB 186 YLAPYVGRQYGRPVDCMAIGVIMYLLSGNPFYEVEDDYENHDKLFRKIAGY 245
 QY 246 EFGSPYWDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGVCAQIE 305
 DB 246 EFGSPYWDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGVCAQIE 305
 QY 78 EFGSPYWDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGVCAQIE 137
 DB 78 EFGSPYWDISQAADLVTRIMEVEQDRIITAEALSHWISGNAASDKNIKXGVCAQIE 137
 QY 306 KNFARAKWKKAIVTTLMKRLRAPEQSTAAQASATDTATGAAGATAAASGATSA 365
 DB 306 KNFARAKWKKAIVTTLMKRLRAPEQSTAAQASATDTATGAAGATAAASGATSA 365
 QY 138 KNFARAKWKKAIVTTLMKRLRAPEQSTAAQASATDTATGAAGATAAASGATSA 197
 DB 138 KNFARAKWKKAIVTTLMKRLRAPEQSTAAQASATDTATGAAGATAAASGATSA 197
 QY 366 PEGDAAPAAKSDNVADPDRSATPATDGSATPATDGSVTPATDGSVTPATDGS 425
 DB 366 PEGDAAPAAKSDNVADPDRSATPATDGSATPATDGSVTPATDGSVTPATDGS 425
 QY 426 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSATPEGATGAPPSK 485
 DB 426 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSATPEGATGAPPSK 485
 QY 258 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSATPEGATGAPPSK 317
 DB 258 ATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPMAAQPDSATPEGATGAPPSK 317
 QY 486 EEAAGYAEQREAS 501
 DB 318 EEAAGYAEQREAS 333

RESULT 11
 Q9YGM4 PRELIMINARY; PRT; 421 AA.
 ID Q9YGM4
 AC Q9YGM4;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Verploegen S., Koenderman L., Coffey P.J.,
 RT "Identification and characterization of CLKIK: a novel granulocyte
 RT Ca2+/calmodulin-dependent kinase."
 RL Blood 0:0-0(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF286366; AA00534.1; -.
 DR HSSP: Q63450; 1A06.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0004648; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_kin_AS.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 357 AA; 40169 MW; 1FA184EFA97FB4 CRC64;
 Query Match 29.9%; Score 771; DB 4; Length 357;
 Best Local Similarity 40.3%; Pred. No. 1,4e-38;
 Matches 148; Conservative 84; Mismatches 109; Indels 26; Gaps 3;
 QY 16 QPSEVTRDLDGVITKEFCEIFRAKDTTGTCKKFGQRDGRKRAKAKEIGILK 75
 DB 15 QMEDIKKEFEKELTGAFSEVLAEEKATGKLFVAKCIPKALGKSSISENIAVL 74
 QY 76 MVKHPNLLVDVPTVRKEVFIFELATGREVDMIDQYSESDTSNVVQVLEAVAY 135
 DB 75 KIKHENIVALLDYESPNNHLYVMQVSGELFDRIYKGFTEKQASTLIRQVLDVAY 134
 QY 136 LHSIKIVHNKLENIYVYNNRLNKSQIVISDFHLAKLE--NGLIKPCGTPPYLAPEV 193
 DB 135 LHMGIYHNDIKPENLLYYSQDESKIMISDFGLSKMEKGVWSTACGTPGYVAPEVLA 194
 QY 194 RQRYGRPVDCMAIGVIMYIILSGNPPFYEVEEDYENHDKNLFKILADYEFDSPYWD 253
 DB 195 QKPYKAVDCWSIGVIAVYIILCGYPPPYDE-----NDSKLFEGQILKAEYEFDSPYWD 246
 QY 254 DISQAADLVTRLMVEQDQRTAEALISHEMISGNAASDKNTKQVCAQIKNFAPAKW 313
 DB 247 DISDAKDFINLMKEDQPNKRYTCEQARHPWLAGDTALNKNIHESVSAQIRKFAKSW 306
 QY 314 KKAIVTTIMKRLRAPEQSSSTAASATDTATPAAGATTAASAGATSAPEDGARA 373
 DB 307 RQAFNATAVVRHNRKHLGSSLDSSNVS-----VSSSLSLASQDCAVY 350
 QY 374 AKSDNYA 380
 DB 351 AKPELS 357
 RESULT 14
 ID 081U85 PRELIMINARY; PRT; 385 AA.
 AC 081U85;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to CamK1-like protein kinase (Cam-kinase I like protein kinase
 DE beta).
 GN CLKIK BETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Verploegen S., Koenderman L., Coffey P.J.,
 RT "Identification and characterization of CLKIK: a novel granulocyte
 RT Ca2+/calmodulin-dependent protein kinase."
 RL Blood 0:0-0(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF286366; AA00534.1; -.
 DR HSSP: Q63450; 1A06.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0004648; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_kin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR kinase.
 SQ SEQUENCE 385 AA; 42913 MW; 717467D019E30FC9 CRC64;
 Query Match 29.7%; Score 767.5; DB 4; Length 385;
 Best Local Similarity 40.4%; Pred. No. 2,6e-38;
 Matches 152; Conservative 79; Mismatches 122; Indels 23; Gaps 5;
 QY 16 QPSEVTRDLDGVITKEFCEIFRAKDTTGTCKKFGQRDGRKRAKAKEIGILK 75
 DB 15 QMEDIKKEFEKELTGAFSEVLAEEKATGKLFVAKCIPKALGKSSISENIAVL 74
 QY 76 MVKHPNLLVDVPTVRKEVFIFELATGREVDMIDQYSESDTSNVVQVLEAVAY 135
 DB 75 KIKHENIVALLDYESPNNHLYVMQVSGELFDRIYKGFTEKQASTLIRQVLDVAY 134
 QY 136 LHSIKIVHNKLENIYVYNNRLNKSQIVISDFHLAKLE--NGLIKPCGTPPYLAPEV 193
 DB 135 LHMGIYHNDIKPENLLYYSQDESKIMISDFGLSKMEKGVWSTACGTPGYVAPEVLA 194
 QY 194 RQRYGRPVDCMAIGVIMYIILSGNPPFYEVEEDYENHDKNLFKILADYEFDSPYWD 253
 DB 195 QKPYKAVDCWSIGVIAVYIILCGYPPPYDE-----NDSKLFEGQILKAEYEFDSPYWD 246
 QY 254 DISQAADLVTRLMVEQDQRTAEALISHEMISGNAASDKNTKQVCAQIKNFAPAKW 313
 DB 247 DISDAKDFINLMKEDQPNKRYTCEQARHPWLAGDTALNKNIHESVSAQIRKFAKSW 306
 QY 314 KKAIVTTIMKRLRAPEQSSSTAASATDTATPAAGATTAASAGATSAPEDGARA 360
 DB 307 RQAFNATAVVRHNRKHLGSSLDSSNVS-----VSSSLSLASQDCAVY 350
 QY 361 GATAPEDGARA 376
 DB 367 GAERPRPTVTAHVS 382

RESULT 15

Q8BW96 PRELIMINARY; PRT; 385 AA.
 AC Q8BW96;
 DT 01-MAR-2003 (Tremblrel, 23, Created)
 DT 01-MAR-2003 (Tremblrel, 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel, 25, Last annotation update)
 DE CANK1-like protein kinase homolog.
 GN E030025C1R1K.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK053173; BAC35285.1;
 DR MGD; MGI:2442190; E030025C1R1K.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR01245; Tyr_kinase.
 DR Pfam; PF00069; kinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00106; PROTEIN KINASE ST; 1.
 SQ SEQUENCE 385 AA; 42945 MW; 320EADCE57A1D55 CRC64;

Query Match 29.7%; Score 767.5; DB 11; Length 385;
 Best Local Similarity 41.3%; Pred. No. 2.6e-38;

Matches 151; Conservative 77; Mismatches 115; Indels 23; Gaps 5;

QY 16 QPSEVTRDYDYGQVKTKEPCEIFRANKDTGKLTCKKQKRDGKVRKAANKNIGILK 75
 DB 15 QAEIDKRIEFKEKETIGTGFSEVLAERKATGKLFAYVCIPKALKKGESEIENEIAYLR 74
 QY 76 MKKEPNILQVADVETREKEVFIFELATGREVPMDLDQGYSPRDTSNVROYLEAVAY 135
 DB 75 KIKENIYALDEDIYESPHNLVYMWQVSGELFRIVEKGYTEKDASTLIRQVLDAVY 134
 QY 136 LHSIKIVHNTKLELVYVNRKSKIVISDFHLAKLE--NGLTKEPCGTPEYLAPVWG 193
 DB 135 LHRNGIYHRDLKPENLVLYSQDESKIVISDFGLSKWEGKDVMTAGTIPGYVAPEVLA 194
 QY 194 KQRYGRPYDCAVIGVIMYLLSGNPPFYEEVEEDYENHDKLFRKILAGDYEPDPSPYMD 253
 DB 195 QKPYSKAVDCWSIGVIAIILGYPFYDE-----NDSKLFEQILKAYEFDSPYMD 246
 QY 254 DISQAQDLVTRLMEVEQDRTLAEBALSHEMISGNAASDNINIKDGVCAQIEKNPARAKW 313
 DB 247 DISDAKDFINLMKEDPNKRYTCQAAHHPMIAGDTALSKNIHESVSAQIRKNFAKSKW 306
 QY 314 KKAIVAVTLTKRLRPE-----QSTAAQS---ASATDTATPGA---AGGATAAAS 360
 DB 307 ROAFNATAVVRMRRLQGSNLDSSNAGVSSNLSLAQKCLAPSTLCSFLSSSSGVAGV 366
 QY 361 GATSAAP 366
 DB 367 GAERP 372

Search completed: April 23, 2004, 15:49:42
 Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:44:58 ; Search time 18 Seconds
(without alignment)
1449.286 Million cell updates/sec

Title: US-10-669-689-2
Perfect score: 2581
Sequence: 1 MFGCVTLGDKKNYNQPSSEV.....SSKGEPAAGYAGDSQREAS 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797.5	30.9	374	1 KCC1_RAT	Q63450 rattus norv
2	793.5	30.7	374	1 KCC1_MOUSE	Q91y58 mus musculu
3	793	30.7	370	1 KCC1_HUMAN	Q14012 homo sapien
4	620.5	24.0	474	1 KCC4_RAT	P13234 rattus norv
5	608	23.6	473	1 KCC4_HUMAN	Q16566 homo sapien
6	602.5	23.3	469	1 KCC4_MOUSE	P08414 mus musculu
7	584.5	22.6	424	1 RPS1_HUMAN	P11801 homo sapien
8	564	21.9	740	1 DCK1_HUMAN	O15075 homo sapien
9	563	21.8	664	1 KCCB_HUMAN	O13554 homo sapien
10	559	21.7	756	1 DCK1_MOUSE	O91188 mus musculu
11	558	21.6	433	1 DCK1_RAT	O08875 rattus norv
12	552	21.4	542	1 KCCB_MOUSE	P08413 mus musculu
13	551	21.3	542	1 KCCB_RAT	P08413 rattus norv
14	542	21.0	527	1 KCCG_RAT	P11730 rattus norv
15	537	20.8	478	1 KCCA_HUMAN	Q09077 homo sapien
16	534	20.7	478	1 KCCA_RAT	P13275 rattus norv
17	530.5	20.6	295	1 KMLC_DICDI	P25333 dictyoscella
18	529.5	20.5	414	1 KCC1_EMENI	Q00771 emericella
19	525	20.3	375	1 KCCA_MOUSE	P11788 mus musculu
20	521	20.2	438	1 KCC1_SCHPO	O9P712 schizosach
21	520.5	20.2	472	1 KCCG_HUMAN	Q13555 homo sapien
22	518	20.1	529	1 KCCG_MOUSE	Q02329 mus musculu
23	517.5	20.1	533	1 KCCD_RAT	P15791 rattus norv
24	507	19.6	382	1 KCC1_METAN	O14458 metathizium
25	494.5	19.2	499	1 KCCD_HUMAN	P53355 homo sapien
26	487.5	18.9	1432	1 DAK1_HUMAN	Q09473 mus musculu
27	487.5	18.9	370	1 DAK1_MOUSE	Q09473 mus musculu
28	486.5	18.8	1442	1 DAK1_MOUSE	Q09473 mus musculu
29	475.5	18.4	370	1 DAK2_HUMAN	Q09473 mus musculu
30	473	18.3	532	1 CDPK_DAUCA	P28512 daucus caro
31	467	18.1	386	1 KPBG_HUMAN	Q28824 bos taurus
32	465	18.0	1176	1 KML5_BOVIN	Q28824 bos taurus
33	463.5	18.0	1906	1 KML5_CHICK	P11799 gallus gall

34	462.5	17.9	386	1 KPBG_RABIT	P00518 oryctolagus
35	462	17.9	610	1 CDP1_ARATH	O06850 arabidopsis
36	462	17.9	1147	1 KML5_RABIT	P29294 oryctolagus
37	461	17.9	580	1 SRK1_SCHPO	O94547 schizosach
38	460	17.8	454	1 DAK3_HUMAN	O43293 homo sapien
39	459.5	17.8	387	1 KPBG_RAT	P13286 rattus norv
40	458	17.7	1914	1 KML5_HUMAN	O15746 homo sapien
41	457	17.7	387	1 KPBG_MOUSE	P07934 mus musculu
42	456.5	17.7	533	1 CDP2_ORYSA	P53683 oryza sativ
43	452.5	17.5	446	1 KCC1_YEAST	P27466 saccharomyc
44	450	17.4	448	1 DAK3_MOUSE	O54784 mus musculu
45	449	17.4	447	1 KCC2_YEAST	P22517 saccharomyc

ALIGNMENTS

RESULT 1
ID KCC1_RAT STANDARD; PRT; 374 AA.
AC Q63450; Q63084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (BC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=94075341; PubMed=8253780;
RA Picciotto M.R., Czernik A.O., Nairn A.C.;
RT "Calcium/calmodulin-dependent protein kinase I. cDNA cloning and
RT identification of autophosphorylation site.";
RL J. Biol. Chem. 268:26512-26521(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RX MEDLINE=95035115; PubMed=7948038;
RA Cho F.S., Phillips K.S., Bogucki B., Weaver T.B.;
RT "Characterization of a rat cDNA clone encoding calcium/calmodulin-
RT dependent protein kinase I.";
RL Biochim. Biophys. Acta 1224:156-160(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF ISOFORM 2.
RC TISSUE=Brain;
RX MEDLINE=96182648; PubMed=8601311;
RA Goldberger J., Nairn A.C., Kuriyan J.;
RT "Structural basis for the autoinhibition of
RT calcium/calmodulin-dependent protein kinase I.";
RL Cell 84:875-887(1996).
CC -1- FUNCTION: Phosphorylates synapsin I.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be
CC phosphorylated to be maximally active.
CC -1- SUBUNIT: Monomer.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=42 kDa;
CC IsoId=Q63450-1; Sequence=Displayed;
CC Name=2; Synonyms=37 kDa;
CC IsoId=Q63450-2; Sequence=VSP_004765;
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
CC subfamily.
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CC -----

DR EMBL; L24907; AAA19670.1; -.

DR EMBL; L26288; AAA66944.1; -.

DR PIR; S50193; S50193.

DR PDB; 1A06; 08-APR-98.

DR PDB; 1MXE; 07-JAN-03.

DR InterPro; IPR000719; Proc Kinase.

DR InterPro; IPR008271; Ser Thr pkin AS.

DR InterPro; IPR002290; Ser Thr pkinase.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Proc Kinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Alternative splicing; 3D-structure.

FT DOMAIN 20 276

FT NP_BIND 26 34

FT BINDING 49 49

FT ACT_SITE 141 141

FT MOD_RES 177 177

FT VARSPPLIC 323 374

FT CONFLICT 112 112

FT CONFLICT 118 118

FT CONFLICT 309 309

FT HELIX 11 12

FT HELIX 16 18

FT TURN 19 19

FT STRAND 20 25

FT STRAND 27 27

FT HELIX 29 33

FT STRAND 34 39

FT TURN 40 42

FT STRAND 45 52

FT HELIX 65 71

FT TURN 72 72

FT TURN 76 77

FT STRAND 78 78

FT STRAND 81 86

FT STRAND 90 95

FT STRAND 102 102

FT HELIX 103 108

FT TURN 109 109

FT HELIX 115 134

FT TURN 135 136

FT HELIX 144 146

FT STRAND 147 149

FT TURN 154 155

FT STRAND 158 160

FT TURN 183 184

FT HELIX 187 190

FT TURN 191 192

FT TURN 197 197

FT HELIX 198 213

FT TURN 223 231

FT TURN 232 233

FT TURN 239 244

FT HELIX 247 256

FT HELIX 261 263

FT HELIX 267 272

FT TURN 274 277

FT TURN 287 297

FT STRAND 302 304

FT STRAND 307 307

FT HELIX 309 315

SO SEQUENCE 374 AA; 41638 MM; 378989BJDFF033AB2 CRC64;

Query Match 30.9%; Score 797.5; DB 1; Length 374;

Best Local Similarity 41.9%; Pred. No. 6,5e-34;

Matches 160; Conservative 73; Mismatches 128; Indels 21; Gaps 4;

QY 14 YNPSRYTBYDYGQVYIKTEEFCEIFRANKDTGKHTQKQKRGKRVKAAKVEIGI 73

DB 10 WKQAEIDRDYDPRDYVGTGAFSEVTLAEDEKRTQKVAKTKAKLAEKESGMEINAV 69

QY 74 LKWKVKNILQVAVTEKREYFIFELATGSEVPDMIDQGYSSRDTSNVVRQVLEAV 133

DB 70 LHKIKPNVIALDDIYESGHLVIMQVSGGLFRIYKRGYTERDASRLIFQVLDVAV 129

QY 134 AYHSLKIYVRNKLKNLYNRLKNSKVISDFHLAKLEN--GLIKPQGYEYIAPVY 191

DB 130 KYLHDLGIYVRDLKPNLLYSLDEDSKIMISDFGLSKMEDPGSVYSTAGTPGYVAPVY 189

QY 192 VGRQRYRPPDCAIGVIMYIILSGNPPFEYEEEDYENHDKNLFKXILAGYERDSY 251

DB 190 LAQPKYSKAVDCWSIGVAVIILCGYPFYDE-----NPAKLEQILKAIEYEDSPY 241

QY 252 WDISQAAXDLVTRLMVEVEDQRTAEBAISHWISGNASDPKNIKDGCAQIEKYPARA 311

DB 242 WDISQAKDFTHLMKPEKRFCEQALQHPWINGDIALDKNIHOSVSEQIKQNFAS 301

QY 312 KWKKAIVVITLMKRLPAPE--QSTAAQASATDTATPGAAGATMAAASGATSAPEGD 369

DB 302 KWKQAFNAIVAVHMKRLQIGTSQEGQGTASHGELLTPTAGSPAGCCCRDCCVEP 358

QY 370 AAPAASDNVAPDRSATPATD 391

DB 359 -----GSELPAPPPSRAMD 374

RESULT 2

KCC1_MOUSE

ID KCC1_MOUSE

AC 091VS8;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)

DE (Cam kinase I).

GN CAMK1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer K.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datschenko L., Marsina K., Farmer A.A., Rubin G.W., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarathne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalhus D.E.,

RA Scherch A., Schein J.B., Jones S.U.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Phosphorylates synapsin I (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.

CC -!- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be

```

CC phosphorylated to be maximally active.
CC -1 SUBUNIT: Monomer (by similarity).
CC -1 SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
CC subfamily.
CC -----
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CC -----
DR EMBL; BC014825; AAH14825.1; -
DR MGD; MGI:1096535; Camk1.
DR GO; GO:0006913; P:nucleocytoplasmic transport; IDA.
DR GO; GO:0007165; P:signal transduction; IDA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; 5_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transfaser; Serine/threonine-protein kinase; Calmodulin-binding;
KW phosphorylation; ATP-binding.
FT DOMAIN 20 276 PROTEIN KINASE.
FT DOMAIN 287 321 CALMODULIN-BINDING (BY SIMILARITY).
FT NP_BIND 26 34 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP (BY SIMILARITY).
FT ACT_SITE 141 141 BY SIMILARITY.
FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 374 AA; 41624 MW; 37889GDA17D3AB2 CRC64;

Query Match 30.7%; Score 793.5; DB 1; Length 374;
Best Local Similarity 41.6%; Pred. No. 1e-33;
Matches 159; Conservative 73; Mismatches 129; Indels 21; Gaps 4

QY 14 YNPSSEVTVDRYDLGGVITKEEFCEIFRAKDTTGGKLATCKKFKORGRKVRKAANEIGI 73
Db 10 WKQMEDIDIDYDFRVLGTGAFSEVTLAEDKRTQLVAIKCAKKALSGKSGMENEIAY 69

QY 74 LKQVKEPIITLDVVFTRKEYFIFLELATGREGVDFWILDCQYSERDTSNVFQVLEAV 133
Db 70 LHKIKPIVIALDIDYESGHHYLIMQVSGGELFDRIVEKGYFERDASRLIFQVLDVAV 129

QY 134 AYHSLSKTVHNLKLENLVYTRKLKSKTIVISDFHLAKLEN--GIKKECGPEYLAEBV 191
Db 130 KYLHDLGVHHDLEKENLLYSLDEDSKIMISDFELSKMEDPGSVLSTACGPIGVAAEBV 189

QY 192 VGRQGRGVPCWMAAGVIMYLLISGNPFVEVEEDVDYENHDKNLFRTKILADYEPDSY 251
Db 190 LAQKYSYSAVDWMSGVIAIYLLCGPPPYDE-----NNAKLFEOILKAEYFSDSY 241

QY 252 WDDISQAADLVTRLMVEBODQRTAEZALSHEWISGNAASDKNIKDCVQAQIEKNIFARA 311
Db 242 WDDISDSAKDFIRHLMKQPEKRFCEQALQHPWLAGDTALDKNIHQSVEBQIKKNFAKS 301

QY 312 KWKCAVRYTTLMKRIAPB--QSSTAAQASATDTATPGAGAGATPAAASGATSPACD 369
Db 302 KWKQAFNATAVVRHNRKIQLTGSGGQGTGSHGILLPTAGAPGAGCCCRDCEVP--- 358

QY 370 AARAAKSDNVAPADRSATPATD 391
Db 359 -----GSELPAPPPSSRAMD 374

RESULT 3
KCC1_HUMAN STANDARD; PRT; 370 AA.
ID KCC1_HUMAN STANDARD; PRT; 370 AA.

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DT 15-JUL-1998 (Ref. 36, Created)
DT 15-JUL-1998 (Ref. 36, Last sequence update)
DT 10-OCT-2003 (Ref. 42, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
DE (CAM kinase I).
GN CAMK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-49.
RX MEDLINE=95369239; Pubmed=7641687;
RA Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D.,
RA Edelman A.M., Snyderman R., Means A.R.;
RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,
domain structure and activation by phosphorylation at threonine-177
by calcium-calmodulin dependent protein kinase I kinase.";
RL EMBO J. 14:3679-3686 (1995).
RL [2]
RP SEQUENCE OF 1-9.
RC TISSUE=platelet;
RX MEDLINE=22608298; Pubmed=12665801;
RA Goemaet R., Goethals W., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003).
CC -1- FUNCTION: Phosphorylates synapsin I.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be
phosphorylated to be maximally active.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK
subfamily.
CC -----
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CC -----
DR EMBL; LA1816; AAA99458.1; -;
DR PIR; S57347; S57347.
DR HSSP; Q63450; 1A06.
DR GeneID; HGNC:1459; CAMK1.
DR MIM; 604998; -;
DR GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. -; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00230; S_TKc_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; calmodulin-binding;
KW phosphorylation; ATP-binding.
FT DOMAIN 20 276 PROTEIN KINASE.
FT DOMAIN 287 321 CALMODULIN-BINDING (BY SIMILARITY).
FT NP_BIND 26 34 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP.
FT ACT_SITE 141 141 BY SIMILARITY.
FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-).
FT MUTAGEN 49 49 K-2A: LOSS OF ACTIVITY.
FT SEQUENCE 370 AA; 41337 MW; 57FA20EBCD0FA76C CRC64;

Query Match 30.7%; Score 793; DB 1; Length 370;
Best Local Similarity 43.7%; Pred. No. 1,1e-33;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;

QY 14 YN0SEVTDRLDGLVITEBCEIFRAKDKTGTGLTKCKFKQKDKKAKKAKNEIGI 73
DB 10 WKQADRIDIDYFRDVLGTGAFSEVILAEKRTQDLVAIKIAENAEKSGKSENEIAY 69
QY 74 LKMYHPNLTQVDFVNRKEFEIFLELATGREVDWTLDDGYSERPTSNNVQVLEAV 133
DB 70 LHKIHPNIVADLDYVESGGHLYLTMQVSGGELFDRIYVEGFYERASRLIFQVLDVAV 129
QY 134 AYHSLKIVHRNLTKEINLYVYRNLKNSKIVISDFHLAKLEN--GLIKEPCTPEYLAPEV 191
DB 130 KYLHDLGIVHRDLKPEENLYISLDEDSKIMISDFLSKMEDEPGSVLSTACCTPGVVAPEV 189
QY 192 VGRQRYGRRPVDCAIGVIMYILISGNPPRYEEVEEDYENHDKULFRKILADYEPDSY 251
DB 190 LAQRYSKAVDCMSIGVILAYILLCGYPPFYDE-----NDAKLFEQILKAYEFPDSY 241
QY 252 WDDISQAKDLVTRLMVEVQDQRTAEALISHEWISGNAADKNIKQVCAQIKENPAPA 311
DB 242 WDDISDASDPIRHMEDKPERKFTCEQALQHPWLAGDTALDKNHQGSBQIKENPKAKS 301
QY 312 KKKKAVRYTTLMKRLRAPE--QSTRAAQSASATDTPGAAGATAAASGATSAP 366
DB 302 KKKQKPNATAVVRHMKIQLGTSGEGGQTAHSGELLTPVAGGAPGACCDCCEP 358

RESULT 4
KCC4_RAT STANDARD; PRT; 474 AA.

AC P13234;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE (EC 2.7.1.123) (Cam kinase-GR) (CamK IV) (Calsepermin).
GN CAMK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
RX MEDLINE=91288548; PubMed=1648230;
RA Ohmsted C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
RT kinase Gr and calsepermin: a gene within a gene.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788 (1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=91304387; PubMed=1649385;
RA Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,
RA Slaughter G.R., Ono T.;
RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
RT cell-specific calmodulin-binding protein are derived from the same
RT gene.";
RT Mol. Cell. Biol. 11:3960-3971 (1991).
RN [3]
RP SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).
RC STRAIN=Spizague-Dawley; TISSUE=Brain;
RX MEDLINE=89174647; PubMed=2538431;
RA Ohmsted C.-A., Jensen K.F., Sahyoun N.;
RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
RT granule cells. Identification of a novel neuronal
RT calmodulin-dependent protein kinase.";
RT J. Biol. Chem. 264:5866-5875 (1989).
RN [4]
RP SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361.
RC STRAIN=Spizague-Dawley;
RX MEDLINE=8913272; PubMed=2914893;

RT "Molecular cloning sequence and distribution of rat calsepermin, a
RT high affinity calmodulin-binding protein.";
RT J. Biol. Chem. 264:2081-2087 (1989).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=96094352; PubMed=7493991;
RA Sun Z., Means R.L., Lemagueresse B., Means A.R.;
RT "Organization and analysis of the complete rat calmodulin-dependent
RT protein kinase IV gene.";
RT J. Biol. Chem. 270:29507-29514 (1995).
CC -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
CC ENRICHED IN CEREBELLAR GRANULE CELLS.
CC -1- FUNCTION: CALSEPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative promoter;
CC Comment=2 isoforms, 1 and 2/Testis-specific, are produced by use
CC of alternative promoters;
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ due to the use of alternative promoters
CC and alternative splicing;
CC Name=1; Synonyms=calcium-calmodulin-dependent protein kinase type
CC IV catalytic chain;
CC IsoId=P13234-1; Sequence=Displayed;
CC Name=2; Synonyms=Calsepermin;
CC IsoId=P13234-2; Sequence=VSP 004789;
CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2
CC is testis specific.
CC -1- PTM: The N-terminus of calsepermin is blocked.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
CC subfamily.
CC -----
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CC -----
DR EMBL: M63334; AAA40865.1; -.
DR EMBL: M74488; AAA40845.1; ALT_SEQ.
DR EMBL: M64757; AAA40856.1; -.
DR EMBL: M64757; AAA40857.1; -.
DR EMBL: J04600; AAA41867.1; -.
DR EMBL: J04446; AAA40990.1; -.
DR PIR: A41103; TVRTCA.
DR HSP: Q63450; 1A06.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS50011; PROTEIN KINASE DM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding; Testis; Alternative splicing;
KW Alternative promoter usage.
FT DOMAIN 42 296 PROTEIN KINASE.
FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT BINDING 71 71 ATP (BY SIMILARITY).
FT ACT_SITE 160 160 BY SIMILARITY.
FT DOMAIN 318 337 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 393 399 POLY-GLU.
FT DOMAIN 403 413 POLY-GLU.
FT VARSPLIC 1 305 Missing (in isoform 2).
FT FTID=VSP 004789.
FT CONFLICT 372 372 I -> M (IN REF. 2 AND 4).
FT SEQUENCE 474 AA; 53133 MW; 56F7AC5644DEBD3 CRC64;

Db 396 SEEVERDAGVEKETSTSMVF-QDPEDELETDDEMKRDSSEKUKSVEEMDPTESEA-- 452

QY 453 ATGAATPEPANAQP--DSTAPE 473

Db 453 -----PDAGLGVPQDADAIOPE 468

RESULT 7

KPSH_HUMAN STANDARD; PRT; 424 AA.

AC P11801; Q9NY19;

DT 01-OCT-1989 (Rel. 12, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serine/threonine-protein kinase H1 (EC 2.7.1.37) (PSK-H1).

GN PSKH1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_Taxid=9606;

OX [1]

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=20541713; PubMed=11087665;

RA Brede G., Solheim J., Troen G., Prydz H.;

RT "Characterization of PSKH1, a novel human protein serine kinase with centrosomal, Golgi, and nuclear localization.";

RL Genomics 70:82-92(2000).

RN [2]

RP SEQUENCE OF 199-348 FROM N.A.

RX MEDLINE=87092414; PubMed=2946189;

RA Hanke S.K.;

RT "Homology probing: identification of cDNA clones encoding members of the protein-serine kinase family.";

RL Proc Natl. Acad. Sci. U.S.A. 84:388-392(1987).

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -1- ENZYME REGULATION: Activity depends on Ca(2+) concentration.

CC -1- SUBCELLULAR LOCATION: Localized in the nucleus with a somewhat compartment, at centrosomes, in the nucleus with a somewhat specter-like presence, and more diffusely in the cytoplasm.

CC -1- TISSUE SPECIFICITY: Expressed in all tissues and cell lines tested with the highest level of abundance in testis.

CC -1- PTM: Autophosphorylated on serine residues.

CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

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CC -----

CC EMBL; AJ272212; CAB91984.1; -

CC EMBL; M14504; AAA36519.1; -

CC PIR; B26368; B26368.

CC HSSP; Q63450; 1A06.

CC Genew; HGNC:9529; PSKH1.

CC MIM; 177015; -

CC GO; GO:0005524; F:ATP binding; NAS.

CC GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.

CC GO; GO:0006468; P:protein amino acid phosphorylation; NAS.

CC InterPro; IPR000719; Prot kinase.

CC InterPro; IPR008271; Ser_Thr_kinase.

CC Pfam; PF00069; Pkinase; 1.

CC ProDom; PD000001; Prot kinase; 1.

CC SMART; SMO0220; S_TKc_1.

CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.

CC PROSITE; PS00108; PROTEIN KINASE_ST; 1.

CC PROSITE; PS00011; PROTEIN KINASE_DOM; 1.

CC Transferrase; Serine/threonine-protein kinase; ATP-binding;

CC Phosphorylation; Golgi stack; Nuclear protein.

FT DOMAIN 98 355

FT NP BIND 104 112

FT BINDING 127 127

FT ACT SITE 218 218

FT MOD RES 380 380

FT MOD RES 381 381

SQ SEQUENCE 424 AA; 48035 MW; B357757DDC1238BD CRC64;

Query Match 22.6%; Score 584.5; DB 1; Length 424;

Best Local Similarity 39.5%; Pred. No. 4.5e-23;

Matches 132; Conservative 67; Mismatches 98; Indels 37; Gaps 8;

QY 20 VTRDYDLGVKITEBFCFEPFAKDKTKGLTKCKFK--RDGRVKAANEIGILKMY 77

Db 94 VTAKIDIALIGRSFSFVAVVEHRAIRQPAIMIKTKRGREVV--CESELRVLRV 150

QY 78 KHPNLLQLVDFVYRKEVFIFLELATGREVDFWILDQGYSESDTSNVQVLEAVAYLH 137

Db 151 RHANILQGVVEFQERVYVWMLATGGLFDRILAKGSFPERDARVLAQVLDGVAYLH 210

QY 138 SUKIVHRNKLLENLYYTRKLSKIVISDFHLA---KLENGLIKPCGPEYLAPEVVG 193

Db 211 ALGITHRDLKEENLLYHPGDSKIIITDFGLASARKGDDCLMKTKTCGPEYLAPEVLA 270

QY 194 RQVRGRPYDCMAIGVIMYLLISGNPPFYEVEEDYENHDKNLPKTLIAGDYEPDSPYWD 253

Db 271 RKPYNVSVDWMLAGVIAILLSTMPF---EDD---NRTRLYQLIRGKISYSGEPWP 322

QY 254 DISQAKDLVTRLMVEVDORITAEATSHWISGNAASD--KNIKGVCAQIKENPFA 311

Db 323 SVSNIAKDFIRLLTVDPGAMTALQALRHVYVSMMASSMKRLH---RSIGN----- 374

QY 312 KWKAARVYTLMLKRLAPEQSGSTAQAASATDT 345

Db 375 -----LLKASRSRQSTKSAQSTRSRST 398

RESULT 8

DCX1_HUMAN STANDARD; PRT; 740 AA.

AC O15075;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.-) (Doublecortin-like and CAM kinase-like 1).

GN DCAMKL1 OR KIAA0369.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=97349984; PubMed=9205841;

RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kocani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

RL DNA Res. 4:141-150(1997).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Retal brain;

RX MEDLINE=9515663; PubMed=10036192;

RA Soseley-Alaoui K., Sivasubava A.K.;

RT "DCAMKL1, a brain-specific transmembrane protein on 13q12.3 that is similar to doublecortin (DCX).";

RL Genomics 56:121-126(1999).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).

RX MEDLINE=98419166; PubMed=9747029;

RA Omori Y., Suzuki M., Ozaki K., Harada Y., Nakamura Y.,

RA Takahashi E.-I., Fujiwara T.;
 RT "Expression and chromosomal localization of KIAA0369, a putative
 RT kinase structurally related to Doublecortin.",
 RL J. Hum. Genet. 43:169-177(1998).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=99162404; PubMed=10051403;
 RA Matsumoto N., Pile D.T., Ledbetter D.H.;
 RT "Genomic structure, chromosomal mapping, and expression pattern of
 RT human DCAMKL1 (KIAA0369), a homologue of DCX (KLI5).";
 RL Genomics 56:179-183(1999).
 CC -1- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
 CC SIGNALING PATHWAY CONTROLLING NEURONAL MIGRATION IN THE DEVELOPING
 CC BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
 CC SYSTEM.
 CC -1- ALTERNATIVE PRODUCTS.
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist. Type A (AS and AL)
 CC and type B (BS and BL) isoforms differ respectively by the
 CC presence or absence of the doublecortin domain. An alternative
 CC splicing occurring in 3' of the mRNA produces the long (L)
 CC instead of the short (S) isoforms;
 CC Name=2; Synonyms=HL;
 CC IsoId=O15075-1; Sequence=Displayed;
 CC Name=1; Synonyms=AS;
 CC IsoId=O15075-2; Sequence=VSP_004907;
 CC Name=3; Synonyms=BS;
 CC IsoId=O15075-3; Sequence=VSP_004905, VSP_004906, VSP_004907;
 CC Name=4; Synonyms=BL;
 CC IsoId=O15075-4; Sequence=VSP_004905, VSP_004906;
 CC -1- TISSUE SPECIFICITY: IN PETAL TISSUES, HIGHLY EXPRESSED IN BRAIN,
 CC DETECTABLE IN LUNG AND LIVER, BUT NOT IN KIDNEY. IN ADULT TISSUES,
 CC EXPRESSED UBICITOUSLY IN THE BRAIN, DETECTABLE IN THE HEART,
 CC LIVER, SPLEEN, THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE
 CC AND COLON. THE TYPE A ISOFORMS SEEM TO BE EXPRESSED PREDOMINANTLY
 CC IN PETAL BRAIN WHEREAS TYPE B ISOFORMS ARE EXPRESSED ABUNDANTLY IN
 CC BOTH PETAL AND ADULT BRAIN.
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
 CC subfamily.
 CC -1- SIMILARITY: Contains 2 doublecortin domains.
 CC -----
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 CC -----
 DR EMBL, AB002367; BAA20824.1; -;
 DR HSSP, Q63450; 1A06.
 DR GeneW, HGNC:2700; DCAMKL1.
 DR MIM, 604742; -;
 DR GO, GO:0005887; C:integral to plasma membrane; TAS.
 DR GO, GO:0004672; F:protein kinase activity; TAS.
 DR GO, GO:0005057; F:receptor signaling protein activity; TAS.
 DR GO, GO:0007417; P:central nervous system development; TAS.
 DR GO, GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro, IPR003533; DCX.
 DR InterPro, IPR000719; Prot_kinase.
 DR InterPro, IPR008271; Ser_Thr_kinase.
 DR InterPro, IPR002290; Ser_Thr_kinase.
 DR Pfam, PF03607; DCX; 2.
 DR Pfam, PF00069; Pkinase; 1.
 DR ProDom, PD000001; Prot_kinase; 1.
 DR SMART, SM00537; DCX; 1.
 DR SMART, SM00220; S_TKc; 1.
 DR PROSITE, PS50309; DC; 2.
 DR PROSITE, PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE, PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE, PS00108; PROTEIN KINASE_CT; 1.
 DR Transfaas, Serine/threonine-protein kinase; ATP-binding; Repeat;
 KW Neogenesis; Alternative splicing.

FT	DOMAIN	57	143	DOUBLECORTIN 1.
FT	DOMAIN	186	269	DOUBLECORTIN 2.
FT	DOMAIN	288	340	SER/PRO-RICH.
FT	DOMAIN	390	647	PROTEIN KINASE.
FT	NP BIND	396	404	ATP (BY SIMILARITY).
FT	BINDING	419	419	ATP (BY SIMILARITY).
FT	ACT SITE	511	511	BY SIMILARITY.
FT	DOMAIN	698	701	POLY-ARG.
FT	VARSPPLIC	1	307	Missing (in isoform 3 and isoform 4).
FT	VARSPPLIC	308	313	/Frid=VSP_004905.
FT	VARSPPLIC	687	740	PASTS -> MLEIE (in isoform 3 and isoform 4).
FT	VARSPPLIC	687	740	/Frid=VSP_004906.
FT	VARSPPLIC	687	740	TTALDKERQVFRFRNRQDVRSRYKQAPAPPEINSESEDYSP
FT	VARSPPLIC	687	740	SSSETVSPNSP -> LNHGFTKSGSLDYQCGMYWI
FT	VARSPPLIC	687	740	RPELIRGRGFSDEDAIRM (in isoform 1 and isoform 3).
FT	VARSPPLIC	687	740	/Frid=VSP_004907.
FT	VARSPPLIC	687	740	SEQUENCE 740 AA; 82223 MW; D7B6D855099A315C CRC64;
FT	VARSPPLIC	687	740	Query Match 21.9%; Score 564; DB 1; Length 740;
FT	VARSPPLIC	687	740	Best Local Similarity 35.6%; Pred. No. 9.2e-22;
FT	VARSPPLIC	687	740	Matches 119; Conservative 65; Mismatches 126; Indels 24; Gaps 4;
QY	11	KKNYNPSEVTDRDYDGVYKTEEPCEIPRAKDRTGKLTCKKFGKRDGRKVRKAARNE	70	
DB	377	EEGFOIPATTEHYKXGRITGDGNFAVKECVERSRAREYALKIKKCKRGKEHIONE	436	
QY	71	IGILKWKHBNILQVDVFTKREYFPLELATGREVPMIDQGYSERDTSNVVRQVL	130	
DB	437	VSLIRKRNHNYLLLEMDVPELYLVNVELVKGDLFALISTNKYTRDASGMLYNLA	496	
QY	131	EAVAYLHSLKTVRNKLNLNLYVNRFLKSK-LVSDFFLAKENGLKEPGCTPEYVLP	189	
DB	497	SAIKYHLSINIVARDIKPENLVLYEHQDSKSLKQDFGLATVDPVLTVCGETPYVAP	556	
QY	190	EAVGRGRYGRPVCMALIGVIMYLLSGNPPYEVEVEDYENHDKVLPRKILAGDYEPFS	249	
DB	557	ELIAETGYGLKVDIMAGVITVLLCGFPFF--RSGDDQE---VLFQILMGQVDFFS	610	
QY	250	PYWDISQAAKDLVTLMEYEDPRTTAEASISHEWISGNAASDKNIKGVCAQIKENPA	309	
DB	611	PYWDNVSQSKELITMLLVVDVQRFSAVQVLEHPVNDGLPENHQLSVAGKIKKHN	670	
QY	310	PAIKKRAVRVTIMKRLRAPEQSGTAAQASAT	343	
DB	671	-----TGPKPNTAAGSVIAT	687	

RESULT 9
 KCCB_HUMAN STANDARD; PRT; 664 AA.
 AC Q13554; Q95437; Q95438; Q95599; Q9UGH7; Q9UGH8; Q9UGH9; Q9UNX0;
 AC Q9UNX7; Q9UP00; Q9Y5M4; Q9Y5P4;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type II beta chain
 DE (EC 2.7.1.123) (Cam-kinase II beta chain) (Cam kinase II beta subunit)
 DE (CamK-II beta subunit).
 GN CAMK2B OR CAMKB OR CAM2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 2, 5, 6 AND 7).
 RC TISSUE=Brain;
 RX MEDLINE=20317016; PubMed=10858498;
 RA Wang P., Wu Y., Zhou T.H., Sun Y., Pei G.;
 RT "Identification of alternative splicing variants of the beta subunit
 RT of human Ca(2+)/calmodulin-dependent protein kinase II with different
 RT activities";

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RL FEBS Lett. 475:107-110(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=Skeletal muscle;
RA Leddy J.J., Salih M., Tuana B.S.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 5).
RC TISSUE=Brain;
RA Li G.Y., Cooper N.G.F.;
RT "Molecular cloning and sequencing of human calcium/calmodulin
RT dependent protein kinase II beta subunit."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 5).
RC TISSUE=Insulinoma;
RX MEDLINE=20277365; PubMed=10819240;
RA Rochlitz H., Voigt A., Lankat-Butterreit B., Goke B., Heimberg H.,
RA Nauck M.A., Schlemann U., Schatz H., Pfeiffer A.F.;
RT "Cloning and quantitative determination of the human
RT Ca2+/calmodulin-dependent protein kinase II (CaMK II) isoforms in
RT human beta cells."
RL Diabetologia 43:465-473(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Lung;
RX MEDLINE=22386257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin C.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Pirange C.,
RA Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 302-603 FROM N.A. (ISOFORM 2).
RX MEDLINE=97214619; PubMed=9060939;
RA Tombes R.M., Krystal G.W.;
RT "Identification of novel human tumor cell-specific CaMK-II variants."
RL Biochem. Biophys. Acta 1355:281-292(1997).
RN [7]
RP FUNCTION: CaM-kinase II (CaMK2) is a prominent kinase in the
RN central nervous system that may function in long-term potentiation
RN and neurotransmitter release.
RN [8]
RP CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
RN [9]
RP KINETIC REGULATION: Autophosphorylation of CaMK2 plays an important
RN role in the regulation of the kinase activity.
RN [10]
RP SUBUNIT: CaMK2 is composed of four different chains: alpha, beta,
RN gamma, and delta. The different isoforms assemble into homo- or
RN heteromultimeric holoenzymes composed of 8 to 12 subunits.
RN [11]
RP ALTERNATIVE PRODUCTS:
RN Event=Alternative splicing; Named isoforms=7;
RN Comment=The variable region of the CaMK2B protein is encoded by
RN at least 7 exons (V1 to V7). Alternative splicing within this
RN region gives rise to CaMK2B isoforms;
RN Name=4;
RN IsoId=Q13554-1; Sequence=Displayed;
RN Name=1; Synonyms=Beta;
RN IsoId=Q13554-2; Sequence=VSP_004776;
RN Name=2; Synonyms=Beta1, Beta'E;
RN IsoId=Q13554-3; Sequence=VSP_004770, VSP_004771, VSP_004775,
CC CC
CC Name=3; Synonyms=Beta2;
CC IsoId=Q13554-4; Sequence=VSP_004770, VSP_004771, VSP_004774,
CC VSP_004776;
CC CC
CC Name=5; Synonyms=Beta4, BetaE;
CC IsoId=Q13554-5; Sequence=VSP_004770, VSP_004771, VSP_004776;
CC Name=6; Synonyms=Beta6;
CC IsoId=Q13554-6; Sequence=VSP_004773, VSP_004776, VSP_004777;
CC Name=7; Synonyms=Beta7;
CC IsoId=Q13554-7; Sequence=VSP_004772, VSP_004776;
CC TISSUE SPECIFICITY: Widely expressed. Expressed in adult and fetal
CC brain. Expression is slightly lower in fetal brain.
CC [1] SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CaMK
CC subfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF078803; AAD42035.1; -
CC EMBL; AF081572; AAD42036.1; -
CC EMBL; AF083419; AAD42038.1; -
CC EMBL; AF081924; AAD42037.1; -
CC EMBL; AF140350; AAD42070.1; -
CC EMBL; U23460; AAC99802.1; -
CC EMBL; AF114272; AAD03744.1; -
CC EMBL; AF112471; AAD03743.1; -
CC EMBL; AJ252236; CAB65120.1; -
CC EMBL; AJ252237; CAB65121.1; -
CC EMBL; AJ252238; CAB65122.1; -
CC EMBL; BC019070; AAH19070.1; -
CC EMBL; U50358; AAB16663.1; -
CC Genew; HGNC:1461; CaMK2B.
CC MIM; 607707; -
CC GO; GO:0004685; F-actin/calmodulin-dependent protein kinase. TAS.
CC GO; GO:0006468; P-protein amino acid phosphorylation; TAS.
CC GO; GO:0007165; Postnatal transduction; TAS.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_Thr_kin_AS.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_GT; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Kinase; Serine/threonine-protein kinase; Calmodulin-binding;
CC Phosphorylation; ATP-binding; Neuron; Alternative splicing.
CC DOMAIN 14 272
CC NP BIND 20 28
CC BINDING 43 43
CC ACT_SITE 136 136
CC DOMAIN 291 301
CC VARSPLIC 316 316
CC FT
CC FT
CC FT
CC FT
CC VARSPLIC 317 340
CC FT
CC FT
CC FT
CC VARSPLIC 316 408
CC FT
CC FT
CC FT
CC VARSPLIC 354 377
CC FT
CC FT
CC FT
CC VARSPLIC 354 392
CC FT
CC FT
CC FT
CC VARSPLIC 379 393
CC FT
CC FT
CC FT
CC VARSPLIC 410 531
CC FT
CC FT
CC FT
CC VARSPLIC 557 582

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FT FT CONFLICT 68 68 /FTID=VSP 004777.
FT FT CONFLICT 533 533 L -> V (IN REF. 3).
SQ SEQUENCE 664 AA; 72726 MW; 9E8C82918D986614 CRC64;

Query Match 21.8%; Score 563; DB 1; Length 664;
Best Local Similarity 31.0%; Pred. No. 9.2e-22;
Matches 157; Conservative 88; Mismatches 181; Indels 80; Gaps 15;

QY 21 TDRYDGLQVYKTEFEIPRAKDITG-----KLTCKKQQRDGRKVKAKNEIGLIK 75
DB 11 TDEYQLYEDIGKGFVSVRRCVLTGHEVAAKIINTKLSARDQKLEREAR-----ICR 66
QY 76 MYKHPIILQVYVFRKKEVFIETELATGEVPMILDDGYISEEDTSNVNQCYLEAVAY 135
DB 67 LKHGSHIVLHDSISEEGFHYLVFDLVGTGELFEDVAEYSEADASHCIQIILEAVLH 126
QY 136 LHSIAKIVHNLKLENIIVYNNRLKNSKIVISDFHLAKLENGLIKE---PGCTPEYLAPRY 192
DB 127 CHOMGVTHHDLPENILLASKCKGAAYKLADFGLAIEVGDDQAMFGFAGTIGYLSPEYL 186
QY 193 GQRYGRPVDCWAGIYIMYITLISGNPFYEVEEEDYENHDKNLPKILAGDYEPSPY 252
DB 187 RKEAYGKPYDIWAGVYITLLVGYPPFYDE-----DQH--KLVOQIKAGVDPSPPEM 238
QY 253 DDISQAKDLVTRIMEVEDQDRTAEBAISHEMI--SGNAASDKNIKQGV-CAQIEKNFA 309
DB 239 DVTVPKAKLIMQMTINPAKRITAEALHFMVOCRSVASMARQETVEC--LKKENA 296
QY 310 RAKMKAVAVITLIMKRLAPBQSTAAQSASATDTATGAGAGATAAASGATAPSGD 369
DB 297 KRKLKALITTLATBNFSVGRQITAPATMST-----AASGTMGLVEQAKLLN-- 346
QY 370 AARAAKSDNVAPADSATPATDGSATPATDGSATPA-----TDGSIATPDGS 417
DB 347 ----KKADEVKQTNSTNSAATSPKGTLPRALEPQTVIHPNPDG--IKSSSDSA 398
QY 418 VTPVDRSATPATDGRATPATBESITVPTQSSAMLATKAATPEPAMQPDSTAFEGA-- 475
DB 399 NTTIEDEDA-----KAPRVDPILSSVRSGSRSGARSGACSPAPFSLPAPS 446
QY 476 -----TGQAPSPSKGEBAQ 490
DB 447 PRISDILNEVRSGSGTPEAEGLSAG 472

RESULT 10
DCK1_MOUSE STANDARD; PRT; 756 AA.
ID DCK1_MOUSE
AC Q9JLM8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase DCKM1 (EC 2.7.1.1-) (Doublecortin-
DE like and CAM kinase-like 1).
GN DCKM1 OR DCLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=20004649; PubMed=10533048;
RA Burgess H.A., Martinez S., Reiner O.,
RT "XIA0369, doublecortin-like kinase, is expressed during brain
RT development."
RL J. Neurosci. Res. 58:567-575(1999).
CC -1- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
CC SIGNALING PATHWAY CONTROLLING NEURONAL MIGRATION IN THE DEVELOPING
CC BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
CC SYSTEM (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Camk

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CC subfamily.
CC -1- SIMILARITY: Contains 2 doublecortin domains.
CC -----
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CC -----
DB EMBL: AF155819; AAF26673.1; -.
DB HSPF: O63450; 1A06.
DB MBD; MGI:1330861; Dcank1.
DB InterPro; IPR003533; DCX.
DB InterPro; IPR000719; Prot_kinase.
DB InterPro; IPR008271; Ser_thr_pkin_AS.
DB InterPro; IPR002290; Ser_thr_pkinase.
DB Pfam; PF03607; DCX; 2.
DB Pfam; PF00069; pkinase; 1.
DB ProDom; PD000001; Prot_kinase; 1.
DB SMART; SM00537; DCX; 2.
DB SMART; SM00220; S_TKc; 1.
DB PROSITE; PS00309; "DC; 2.
DB PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DB PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DB Transferrase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Neurogenesis.
FT DOMAIN 57 143 DOUBLECORTIN 1.
FT FT 186 269 DOUBLECORTIN 2.
FT DOMAIN 298 358 SER/PRO-RICH.
FT DOMAIN 406 663 PROTEIN_KINASE.
FT NP_BIND 412 420 ATP (BY SIMILARITY).
FT BINDING 435 435 ATP (BY SIMILARITY).
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 756 AA; 84153 MW; 3D1DF18C23129F2 CRC64;

Query Match 21.7%; Score 559; DB 1; Length 756;
Best Local Similarity 35.6%; Pred. No. 1.7e-21;
Matches 119; Conservative 63; Mismatches 128; Indels 24; Gaps 4;

QY 11 KKNYQSEVTDYDIDQVYKTEFEIPRAKDITGKLTCKKQQRDGRKVKAKNE 70
DB 393 EESGQIPATITETERYKGRITGDNFVAVKCIERSTAREVALKIIKSKRGKHEHNIQ 452
QY 71 IGIKMKVHPNIIQLYDVFTKREYFIETELATGEVPMILDDGYISEEDTSNVNQCYLE 130
DB 453 VSIIRVYKHENIYLLIEMDVPTLEYLVMLVKGDLFPALITSTKXTERDASGMYNFA 512
QY 131 EAVAYHSLKIVHNLKLENIIVYNNRLKNSK-IVISDFHLAKLENGLIKEPGTPEYLAP 189
DB 513 SAIRYLSLNIYHVDLPENILLASKCKGATGFGLATVDDPLTYVCGTPTVYVAP 572
QY 190 EWVGRQGRPVDCWAGIYIMYITLISGNPFYEVEEEDYENHDKNLPKILAGDYEPFS 249
DB 573 EIIAFETGYGKVDIMAGVYITLLCGFPF--RSGGDDOE-----VLFQIILMGVDFPS 626
QY 250 PYWDDISQAKDLVTRIMEVEDQDRTAEBAISHEMIISGNAASDKNIKQGVCAQIEKNFA 309
DB 627 PYWDDVSDSAKELINMLLVNVDQFSAVGVLEHPWVNDGLPENHQSVAQIKIKHEN 686
QY 310 RAKMKAVAVITLIMKRLAPBQSTAAQSASAT 343
DB 687 -----TGPKPSTAAGVSVIAT 703

RESULT 11
DCK1_RAT STANDARD; PRT; 433 AA.
ID DCK1_RAT
AC O08875;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DE      30-MAY-2000 (Rel. 39, Last annotation update)
DR      Serine/threonine-protein kinase DCAKML1 (EC 2.7.1.-) (Doublecortin-
DE      like and CAM kinase-like 1) (Calcium/calmodulin-dependent protein
DE      kinase type 1-like CPG16).
GN      DCAKML1 OR CPG16.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCST_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Miscar;
RX      MEDLINE=98364306; PubMed=9699150;
RA      Heyroni D., Ratner A., Bundman W., Lederfein D., Gaberah A.,
RA      Mangels W., Silverman M.A., Kedari H., Naor C., Kornuc M., Hanoch T.,
RA      Seger R., Thelliel L.E., Nedivi E., Richter-Levin G., Clitri Y.;
RT      "Hippocampal plasticity involves extensive gene induction and multiple
RT      cellular mechanisms."
RL      J. Mol. Neurosci. 10:75-98(1998).
CC      -I- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCITRI-
CC      SIGNALING PATHWAY CONTROLLING NEURONAL MIGRATION IN THE DEVELOPING
CC      BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
CC      SYSTEM (BY SIMILARITY).
CC      -I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Camk
CC      subfamily.
CC      -----
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CC      or send an email to licenses@isb-sib.ch).
CC      -----
DR      EMBL; U78857; AAC9476.f.1; -.
DR      HSSP; O63450; 1A06.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR008271; Ser_thr_pkin_AS.
DR      InterPro; IPR002290; Ser_thr_pkinase.
DR      Pfam; PF00069; Pkinase; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SMO0220; S_TKC_1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KM      Transferrase; Serine/threonine-protein kinase; ATP-binding;
KM      Neurogenesis.
FT      DOMAIN          1       33     SER/PRO-RICH (BY SIMILARITY).
FT      DOMAIN          83      340    PROTEIN KINASE.
FT      NP_BIND         391      394    POLY-ARG.
FT      NP_BIND         89        97    ATP (BY SIMILARITY).
FT      BINDING        112      112    ATP (BY SIMILARITY).
FT      ACT_SITE       204        204    BY SIMILARITY.
SQ      SEQUENCE      433 AA; 47680 MW; 0CE5BE06E152A557D CXC64;

Query Match      21.6%; Score 558; DB 1; Length 433;
Best Local Similarity 35.7%; Pred. No. 1e-21;
Matches 119; Conservative 62; Mismatches 128; Indels 24; Gaps 4;

QY      12 KNNQPSSEVVDRLDGVYIKFEFCEIFRAQDKTTGKHHTKKQKRDGRKVRRAANKET 71
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DY      191 VVGQRGRPRPYDCALIGYIMTLISGNPPFEVEEBDDYENHDKNLFKKIIAGDYEPDSP 250

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Db      251  IIAETGYGKAVDIMAAGVITTYLLCGFPF--RSGBDQE-----VLEFDGLMGQVDFPSP 30
Oy      251  YNDIDIOAAKLDVTRLMVEYDQDRTITAEALISHWISGNAPSDKNITKDYCAQIEKNFAR 310
Db      305  YMNVSVDASAKELINMMLLVNVDQSFSAQVLEHFWVNDGLFENHQLSVAGRIKGFNF- 363
Oy      311  AKMKKAVRTTLMKRLRAPESGSTTAAQSASAT 343
Db      364  -----TGKPSSTDAQSVIAT 390

RESULT 12
KCB_MOUSE
ID_KCB_MOUSE STANDARD; PRT; 542 AA.
AC P26852;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II beta chain
DE (EC 2.7.1.123) (Cam-kinase II beta chain) (Cam kinase II beta subunit)
DE (CamK-II beta subunit).
GN CAMK2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_FastID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=92334366; Pubmed=132143;
RA Karls U., Mueller U., Gilbert D.T., Copeland N.G., Jenkins N.A.,
RA Harbers K.;
RT "structure, expression, and chromosomal location of the gene for the
RT beta subunit of brain-specific Ca2+/calmodulin-dependent protein
RT kinase II identified by transgene integration in an embryonic lethal
RT mouse mutant".
RL Mol. Cell. Biol. 12:3644-3652(1992).
CC
CC -1- FUNCTION: Cam-kinase II (CAMK2) is a prominent kinase in the
CC central nervous system that may function in long-term potentiation
CC and neurotransmitter release.
CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Autophosphorylation of CAMK2 plays an important
CC role in the regulation of the kinase activity.
CC -1- SUBUNIT: CAMK2 is composed of four different chains: alpha, beta,
CC gamma, and delta. The different isoforms assemble into homo- or
CC heteromultimeric holoenzymes composed of 8 to 12 subunits.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK
CC subfamily.
CC
CC -----
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CC
CC EMBL: X63615; CAA45160.1; -.
DR PIR; A45025; A45025.
DR HSSP; Q63450; LA06.
DR MGSP; MG1:88257; CamK2b.
DR InterPro; IPR000719; Ser_Pkin_AS.
DR InterPro; IPR008271; Ser_Ehr_Pkin_AS.
DR InterPro; IPR002290; Ser_thr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PDO00001; Proc_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase, Serine/threonine-protein kinase, Calmodulin-binding;
KW Phosphorylation; ATP-binding; Neurone.
KW DOMAIN 14 272 PROTEIN KINASE.
KW

```

FT NP BIND 20 28 ATP (BY SIMILARITY).
 FT BINDING 43 43 ATP (BY SIMILARITY).
 FT ACT SITE 136 136 BY SIMILARITY.
 FT DOMAIN 291 301 CALMODULIN-BINDING.
 SQ SEQUENCE 542 AA; 60475 MW; 8A7962A62D7075D0 CRC64;

Query Match 21.4%; Score 552; DB 1; Length 542;
 Best Local Similarity 32.7%; Pred. No. 2.6e-21;
 Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

21 TDYDGLGVYKTEEFCEIFRAKDKTTG-----KLTCKCKQKQKDRKRYKAANEIGLK 75
 11 TDEYQLYEETIGKAFSVVRCKYKLTGHEHYAAKIINTKLSARDKQKLEERAR----ICR 66
 76 MWKHPNITLQVDFVTRKEVFIFLELATGREVDFWILIDOGYSEBDTSNVVRQVLEAVAY 135
 67 LKHSNIVRLHDSISEGFHYLVFPLDTGTGELFEDIVAREYSEADASHCIGQILEAVLH 126
 136 LHSKLVHRLKLENIIVYNNRLKSKIVISDFHLAKLENGLIKE--PCGTPEYLAPEVY 192
 127 CHQMGVVRHDLKRENILLASKCKGAAYKLADFLAIEVQGDQAWFGFAGTGYLSPEVL 186
 193 GRQRYGPRVDCALIGVIMYLLSGNPPFYSEVEDDYENHDKLFRKILAGYEPSPYV 252
 187 RKEAYGKRPVDMACGVILYLLVGYPPFWDE-----DQH--KLXQKIKAGAYDPSPSEW 238
 253 DDISQAKDLVTLMVEEDQORITAEATISEHMI--SGNAASDKNIKQGV-CAQIEKNFA 309
 239 DVTPEAKNLINQMLTINPAKRIITAEHALKHPVQCRSVASMHROETVEG--LKKNFA 296
 310 RAKWKAVVETTLMKRLAPESSTAAQASATDTATPGAGATPAAASGATSAPEGD 369
 297 RRLKGAIIITMLATRNFSVGRQTAPATMST-----AASGTMGVLEQAKSLN-- 346
 370 AARAKSDNVAPADRSATPATDGSATPATDGSVTPA-----TDGSIPTATDGS 417
 347 ----KKADGVKPTNS--TKNSSATISPKGSLPPALBPQTIVHNPVG-IKSSDST 398
 418 VTPVTRSATPATDGRATPATSESTVPTTQ 447
 399 NTTIEDDA-----KARKOEIIKYTE 419

RESULT 13

KCCB_RAT STANDARD; PRT; 542 AA.

AC P08413; 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Calcium/calmodulin-dependent protein kinase type II beta chain
 (EC 2.7.1.123) (Cam-kinase II beta chain) (Cam kinase II beta subunit)

DE (CamK-II beta subunit).

OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCB1_TaxID=10116;
 (1) _____

RN SEQUENCE FROM N.A.

RC TISSUE=Brain;
 MEDLINE=87175563; PubMed=3470758;

RA Bennett M.K., Kennedy M.B.;
 RT "Deduced primary structure of the beta subunit of brain type II
 RT Ca2+/calmodulin-dependent protein kinase determined by molecular
 RT cloning.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:1794-1798 (1987).

CC -1- FUNCTION: Cam-kinase II (CAMK2) is a prominent kinase in the
 CC central nervous system that may function in long-term potentiation
 CC and neurotransmitter release.

CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
 CC -1- ENZYME REGULATION: Autophosphorylation of CAMK2 plays an important
 CC role in the regulation of the kinase activity.

CC -1- SUBUNIT: CAMK2 is composed of four different chains: alpha, beta,
 CC gamma, and delta. The different isoforms assemble into homo- or
 CC heteromultimeric holoenzymes composed of 8 to 12 subunits.
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
 CC subfamily.

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DR EMBL; M16112; AAA1866.1; -.
 DR PIR; A26464; A26464.
 DR HSRP; Q63450; 1A06.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW Phosphorylation; ATP-binding; Neurone.
 FT DOMAIN 14 272
 FT NP_BIND 20 28
 FT BINDING 43 43
 FT ACT_SITE 136 136
 FT DOMAIN 291 301
 SQ SEQUENCE 542 AA; 60401 MW; 8A7962A64A930D0 CRC64;

Query Match 21.3%; Score 551; DB 1; Length 542;
 Best Local Similarity 32.7%; Pred. No. 3e-21;
 Matches 147; Conservative 83; Mismatches 156; Indels 64; Gaps 14;

21 TDYDGLGVYKTEEFCEIFRAKDKTTG-----KLTCKCKQKQKDRKRYKAANEIGLK 75
 11 TDEYQLYEETIGKAFSVVRCKYKLTGHEHYAAKIINTKLSARDKQKLEERAR----ICR 66
 76 MWKHPNITLQVDFVTRKEVFIFLELATGREVDFWILIDOGYSEBDTSNVVRQVLEAVAY 135
 67 LKHSNIVRLHDSISEGFHYLVFPLDTGTGELFEDIVAREYSEADASHCIGQILEAVLH 126
 136 LHSKLVHRLKLENIIVYNNRLKSKIVISDFHLAKLENGLIKE--PCGTPEYLAPEVY 192
 127 CHQMGVVRHDLKRENILLASKCKGAAYKLADFLAIEVQGDQAWFGFAGTGYLSPEVL 186
 193 GRQRYGPRVDCALIGVIMYLLSGNPPFYSEVEDDYENHDKLFRKILAGYEPSPYV 252
 187 RKEAYGKRPVDMACGVILYLLVGYPPFWDE-----DQH--KLXQKIKAGAYDPSPSEW 238
 253 DDISQAKDLVTLMVEEDQORITAEATISEHMI--SGNAASDKNIKQGV-CAQIEKNFA 309
 239 DVTPEAKNLINQMLTINPAKRIITAEHALKHPVQCRSVASMHROETVEG--LKKNFA 296
 310 RAKWKAVVETTLMKRLAPESSTAAQASATDTATPGAGATPAAASGATSAPEGD 369
 297 RRLKGAIIITMLATRNFSVGRQTAPATMST-----AASGTMGVLEQAKSLN-- 346
 370 AARAKSDNVAPADRSATPATDGSATPATDGSVTPA-----TDGSIPTATDGS 417
 347 ----KKADGVKPTNS--TKNSSATISPKGSLPPALBPQTIVHNPVG-IKSSDST 398
 418 VTPVTRSATPATDGRATPATSESTVPTTQ 447
 399 NTTIEDDA-----KARKOEIIKYTE 419

RESULT 14

KCCG RAT STANDARD; PRT; 527 AA.

AC P11730; 064003; 064004;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type II gamma chain
 (EC 2.7.1.123) (Cam-kinase II gamma chain) (Cam kinase II gamma
 subunit) (CaMK-II gamma subunit).
 GN CAMK2G.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain;
 RX MEDLINE=89034067; PubMed=2846534;
 RA Tominatsu T., Kameshita I., Fujisawa H.;
 RT "Molecular cloning of the cDNA encoding the third polypeptide (gamma)
 of brain calmodulin-dependent protein kinase II.";
 RL J. Biol. Chem. 263:16082-16086(1988).
 RT [2]
 RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
 RC TISSUE=Aortic smooth muscle;
 RX MEDLINE=94226614; PubMed=8172610;
 RA Zhou Z.L., Ikebe M.;
 RT "New isoforms of Ca2+/calmodulin-dependent protein kinase II in
 smooth muscle.";
 RL Biochem. J. 299:489-495(1994).
 CC -1- FUNCTION: Cam-kinase II (CAMK2) is a prominent kinase in the
 central nervous system that may function in long-term potentiation
 and neurotransmitter release.
 CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
 CC -1- ENZYME REGULATION: Autophosphorylation of CAMK2 plays an important
 role in the regulation of the kinase activity.
 CC -1- SUBUNIT: CAMK2 is composed of four different chains: alpha, beta,
 gamma, and delta. The different isoforms assemble into homo- or
 heteromultimeric holoenzymes composed of 8 to 12 subunits.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=A;
 CC IsoId=P11730-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P11730-2; Sequence=VSP_004781, VSP_004782;
 CC Name=C;
 CC IsoId=P11730-3; Sequence=VSP_004781, VSP_004783;
 CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
 subfamily.
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC -----
 CC EMBL; J04063; AAA41857.1; -;
 CC EMBL; S71570; AAB30670.1; -;
 CC EMBL; S71570; AAB30671.1; -;
 CC PIR; A31908; A31908.
 CC HSP; Q63450; 1A06.
 CC InterPro; IPR000719; Prot. kinase.
 CC InterPro; IPR008271; Ser_thr_pkin_AS.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; Pkinase; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00220; S_TKC_1.
 CC SMART; SM00220; S_TKC_1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.

KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KM Phosphorylation; ATP-binding; Neutrone; Alternative splicing.
 FT DOMAIN 14 272
 FT NP_BIND 20 28
 FT BINDING 43 43
 FT ACT_SITE 136 136
 FT DOMAIN 291 301
 FT VARSPPLIC 316 336
 FT VARSPPLIC 351 361
 FT VARSPPLIC 351 361
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 FT CONFLICT 2 2
 FT SEQUENCE 527 AA; 59038 MW; 58DBF1B72F64FA31 CRC64;
 SQ
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 Best Local Similarity 34.4%; Pred. No. 8.2e-21;
 Matches 141; Conservative 77; Mismatches 146; Indels 46; Gaps 13;
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 DB 11 TDDYQLFEELGKGFVSVRCKVKTSTQEVAAKINTKLSARPHQKLEARE-----ICR 66
 QY 76 MKKPNIIQLVDVFTKREYIFLELATGREVPWILDQGYISERDTSNVYQVLENAVY 135
 DB 67 LKHPNIVRLHDSISEGPHYLVPDLVGLGELFEDIVAREYSEADASHCHQILIESVNH 126
 QY 136 LHSIKIVRNKLENTLVYVNLKNSKIYISDFHLAKLENGIKSP-----CGTPEYIAP 189
 DB 127 IHQHDIVRHDLKPELNLASCKGAAYKLADFGLAIEVQG---EQQAFGAGTPIGYISF 183
 QY 190 EYVGRGVRGPRVDCVAIGVIMYLLSGNPPEYEEYEDDYENHDKLPRKILAGYEDFS 249
 DB 184 EYLRKDPGKPRVDIACGVIIYLLVGPFPWDE-----DQH--KLYQQLKAGAYDPFS 235
 QY 250 PYWDDISQAKDLVTRLMVEBDDQRTLEBAISHWT--SGNAASDKNIKGV-CAQIEK 306
 DB 236 PEMDTVTTEBAKLLINQMILINPAKRITADQALKHPWCQRSTVASMGRCEVTEC--LRK 293
 QY 307 NPARAKMKKAVRVITLMGR-LRAPQSTAAQASADTATPGAGATATAAASGATSA 365
 DB 294 FNAARKLKGALITTLVSRNFSVGRQSSAPASPAAS-----AAGLAGQAASLANKK 345
 QY 366 PEGDABARAKSDNVAPADRSATPATDGSATPATDGSATTPATD 415
 DB 346 SDGIVYKRRKSSSVHLMPEQTIVVHN-----ATDG-INGTSBSCNTTDD 389
 RESULT 15
 ID KCCA HUMAN STANDARD; PRT; 478 AA.
 AC Q9UQW7; Q9Y352;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type II alpha chain
 (EC 2.7.1.123) (Cam-kinase II alpha chain) (Cam kinase II alpha
 subunit) (CaMK-II alpha subunit).
 GN CAMK2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC TISSUE=Brain;
 RA Li G.Y., Cooper N.G.F.;
 RT "Human calcium/calmodulin-dependent protein kinase II: cDNA cloning
 and gene analysis.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

central nervous system that may function in long-term potentiation
and neurotransmitter release.
CC CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Autophosphorylation of Thr-286 allows the
CC kinase to switch from a calmodulin-dependent to a calmodulin-
CC independent state (By similarity).
CC -1- SUBUNIT: CAMK2 is composed of four different chains: alpha, beta,
CC gamma, and delta. The different isoforms assemble into homo- or
CC heteromultimeric holoenzymes composed of 8 to 12 subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=C9UCM7-1; Sequence=Displayed;
CC Name=B;
CC IsoId=G9UCM7-2; Sequence=VSP 004766;
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMK
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL; AF145710; AAD30558.1; -;
CC EMBL; AF145711; AAD30559.1; -;
CC HSSP; O63450; 1A06.
CC Genew; HGNC:1460; CAMK2A.
CC MIM; 114078; -;
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_Thr_kin_AS.
CC InterPro; IPR002290; Ser_Thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
CC Phosphorylation; ATP-binding; Alternative splicing.
CC FT DOMAIN 13 271
CC NP_BIND 19 27
CC BINDING 42 42
CC ACT_SITE 135 135
CC MOD_RES 286 286
CC DOMAIN 290 300
CC VARSPIC 328 328
CC /FTId=VSP_004766.
CC /FTId=VSP_004766.
CC SQ SEQUENCE 478 AA; 54029 MW; 10800A85CAD724BB CRC64;
Query Match 20.8%; Score 537; DB 1; Length 478;
Best Local Similarity 32.3%; Pred. No. 1.3e-20;
Matches 137; Conservative 74; Mismatches 141; Indels 72; Gaps 12;
QY 21 TDRYDLQGVITKEEFCEIFR-----AKDKTTGKLTCKFKQKDGKRVKKAANEIGILK 75
DB 10 TEEYQLPEELGKAFSVRRGVKVLAGEYAAKIINTKKLSARDHOKLEREAR-----ICR 65
QY 76 MTKHFNILQVDVFTVTKKEFIFLELATGREVDWILDQGYSERDTSNVVRYOLEAVAY 135
DB 66 LKXHPNIVRLHDS;SERGHHYLLIFDLVTGGELFEDIYAREYSEADSHCTIQILRAVLH 125
QY 136 LHSKIYHRNKLKENTLYYRNKLNSKIVISDFHLAKLNLGLKEP-----CGTPEYIAP 189
DB 126 CHQGVVVRHDLKPEFNLLASLKGAAVYKADFGIALIVEG---EQAMRFGAGTPLYLP 182
QY 190 EVVGRQRYGRPVDCMAGIVMYILLGNPPYEEVEDDYENDKMLFRKILAGDYEFDS 249
DB 183 EVLRKDKYGRKVDLMACGVILYLLVGVPPFWDE-----DQH--RLYQGIKAGAYDFPS 234

DB 235 PEMDVTTPKADLIRKMLTINSKRITAAELKHEWISHRSVVASCMERQETVDC--LKK 292
QY 307 NFAPAKKKKAVRVTTLMKRLRAPESSTPAASASATDTATPGAAAGATMAAASGATSAP 366
DB 293 FNARRRLKGAILTTLW-----ATNFGSGKSGG----- 320
QY 367 EGDAPAAASDVVAPADRSATPATDGSATPATDGSVTPATDGSITPATDG---SVTPYTD 423
DB 321 -----NKSIDGVKSSSESTNTTIDEDTKVAKKEIIVTEQLIAISNGPSESTIMCD 374
QY 424 RSAT 427
DB 375 PGMT 378

Search completed: April 23, 2004, 15:48:43
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:49:49 ; Search time 48 Seconds
(without alignments)
2885.710 Million cell updates/sec

Title: US-10-669-689-2
Perfect score: 2581
Sequence: 1 MPFGCTTLDKKNYNQPSSEV.....SSKGEHAGYAGDSQREAS 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2581	100.0	501	12	US-10-669-689-2
2	2581	100.0	501	13	US-10-153-921-2
3	2577	99.8	501	9	US-09-797-039-2
4	2577	99.8	501	12	US-10-423-643-19
5	2577	99.8	501	14	US-10-170-789-2
6	2577	99.8	501	15	US-10-085-198-6
7	2577	99.8	501	15	US-10-258-106-17
8	2402.5	93.1	473	12	US-10-425-114-54473
9	2402.5	93.1	473	12	US-10-425-114-54473
10	1457.5	56.5	317	12	US-10-425-114-54471
11	966	37.4	204	11	US-09-764-875-725
12	852	33.0	219	9	US-09-764-868-832
13	852	33.0	219	11	US-09-764-875-1035
14	793	30.7	370	10	US-09-817-181-4
15	793	30.7	370	10	US-09-769-970-19

16	793	30.7	370	14	US-10-142-356-7	Sequence 7, Appli
17	793	30.7	370	14	US-10-300-828-4	Sequence 4, Appli
18	793	30.7	370	14	US-10-090-002-4	Sequence 4, Appli
19	793	30.7	370	14	US-10-204-041-10	Sequence 10, Appli
20	771	29.9	317	10	US-09-935-464-36	Sequence 36, Appli
21	771	29.9	317	14	US-10-125-835-36	Sequence 36, Appli
22	771	29.9	357	14	US-10-024-0368-2	Sequence 2, Appli
23	771	29.9	357	15	US-10-258-106-2	Sequence 2, Appli
24	767.5	29.7	385	15	US-10-446-175-2	Sequence 2, Appli
25	764	29.6	355	14	US-10-355-975-10	Sequence 10, Appli
26	764	29.6	355	15	US-10-258-106-11	Sequence 11, Appli
27	754.5	29.2	356	15	US-10-446-175-4	Sequence 4, Appli
28	747.5	29.0	476	10	US-09-935-464-3	Sequence 5, Appli
29	747.5	29.0	476	12	US-09-960-443-2	Sequence 4, Appli
30	747.5	29.0	476	12	US-10-380-235-4	Sequence 4, Appli
31	747.5	29.0	476	14	US-10-125-835-5	Sequence 5, Appli
32	746	28.9	460	10	US-09-935-464-3	Sequence 3, Appli
33	746	28.9	460	14	US-10-125-835-3	Sequence 3, Appli
34	718	27.8	326	9	US-09-817-181-2	Sequence 2, Appli
35	718	27.8	326	14	US-10-300-828-2	Sequence 2, Appli
36	718	27.8	326	14	US-10-090-002-2	Sequence 2, Appli
37	699.5	27.1	484	12	US-10-425-114-54130	Sequence 16, Appli
38	650	25.2	280	9	US-09-835-788A-16	Sequence 16, Appli
39	650	25.2	280	14	US-10-175-042-16	Sequence 16, Appli
40	645.5	25.0	310	15	US-10-369-493-5955	Sequence 5955, Ap
41	642.5	24.9	343	10	US-09-769-970-5	Sequence 5, Appli
42	608	23.6	473	14	US-10-320-351-15	Sequence 15, Appli
43	608	23.6	473	15	US-10-116-275-153	Sequence 153, App
44	607	23.5	298	12	US-10-220-120-240	Sequence 240, App
45	584.5	22.6	424	12	US-10-072-012-330	Sequence 330, App

ALIGNMENTS

RESULT 1
US-10-669-689-2
; Sequence 2, Application US/10669689
; Publication No. US20040038363A1
; GENERAL INFORMATION:
; APPLICANT: VAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00612DVI
; CURRENT APPLICATION NUMBER: US/10/669,689
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-689-2

Query Match 100.0%; Score 2581; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.8e-160;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFGCTTLDKKNYNQPSSEVTDRIYDLGVYKTEECETFRADKTKTGKLNCKKFOKDDG 60
DB 1 MPFGCTTLDKKNYNQPSSEVTDRIYDLGVYKTEECETFRADKTKTGKLNCKKFOKDDG 60
QY 61 KKKRAKKEIGILKKVKKPNILQVDVFTKEFFIFLATGREGVPMIDGGYSER 120
DB 61 KKKRAKKEIGILKKVKKPNILQVDVFTKEFFIFLATGREGVPMIDGGYSER 120
QY 121 DTSNVKQVLEAVAYLSIKIVHRNLKLENLYNNRLKNSKIVISDFHLAKLENGIIEP 180
DB 121 DTSNVKQVLEAVAYLSIKIVHRNLKLENLYNNRLKNSKIVISDFHLAKLENGIIEP 180

D	b		12	DTSNVRQYLZAAVAYLHSLKIVHRLLKLENIWYRLNKSXIVISDPHLAKLENGLIKPEP	186
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D	b		181	CGFEFLAEAVVGRRQRYGPRVDCMAIGVMYILLSGNPFFEEVEEDDYENHDKNLFRI	240
Q	y		241	LAGDYEFDEBPYMDISQAACKLVPLTLMVEEODQRTLEBAISHWISGNAASDKNIKDG	300
D	b		241	LAGDYEFDBPYMDISQAACKLVPLTLMVEEQDQRTLEBAISHWISGNAASDKNIKDG	300
Q	y		301	CAGIEKNFPARAKWKCAVRVTTIMKLRLAPEOSTAAGSASTDTATPGGAAGATAAAS	360
D	b		301	CAGIEKNFPARAKWKCAVRVTTIMKRLRAPESGSTAAQSABATLTATPGAAGATAAAS	360
Q	y		361	GATSAPEGDAAPRAASDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP	420
D	b		361	GATSAPEGDAAPRAASKDNVAPADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP	420
Q	y		421	VYDRSATPATDGRATPATTEESTVPTTOSAMLATTAATPPPAACPDSTAPBEGATGOAP	480
D	b		421	VYDRSATPATDGRATPATTEESTVPTTOSAMLATTAATPPPAACPDSTAPBEGATGOAP	480
Q	y		481	PSSKGEEAAGYAQESOREEAS	501
D	b		481	PSSKGEEAAGYAQESOREEAS	501

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RESULT 2
US-10-153-921-2
; Sequence 2, Application US/10153921
; Publication No. US20020142430A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000612D1V
; CURRENT APPLICATION NUMBER: US/10/153,921
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-10-153-921-2

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Query Match	100.0%;	Score 2581;	DB 13;	Length 501;
Best Local Similarity	100.0%;	Pred. No. 1.8e-160;		
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Qy	61 RKRKRAKAKNETGILLKVKKHPNLLQVADVTVTRKEVFIETLATGAREVFDMLDGGYSER	120
Db	61 RKRKRAKAKNETGILLKVKKHPNLLQVADVTVTRKEVFIETLATGAREVFDMLDGGYSER	120
Qy	121 DTSNVVRQVLEAAVAYLHSKTIYHRNKLKENTLVYVYRLNLSKTIVISDFHLATLNGLTKEP	180
Db	121 DTSNVVRQVLEAAVAYLHSKTIYHRNKLKENTLVYVYRLNLSKTIVISDFHLATLNGLTKEP	180
Qy	181 CGRPETLAPRVVGRQKRGPRVDCMAIGVMTLLSGNPFYEVEEEDDYENHNDNLPKTI	240
Db	181 CGRPETLAPRVVGRQKRGPRVDCMAIGVMTLLSGNPFYEVEEEDDYENHNDNLPKTI	240
Qy	241 LAGDYEFDSFYWMDISQAADLVTRLIMEVEODORTTAAEASHHEWISGNAASDNKINDGV	300

	Accession	Protein	Length
Db	244	LAGDVEFDSPYDDISQPAKLVLRIMVEVEDQRIITEEBAISHEMIISGNASPKNIKDG	3600
Qy	301	CAQIENENPARAKCKKAVVTTLMKRLPAPEOSSSTPAASQASADTDTAPGAAGATAAAS	360
Db	301	CAQIENENPARAKCKKAVVTTLMKRLPAPEOSSSTPAASQASADTDTAPGAAGATAAAS	360
Qy	361	GATSAEEDGAPAAAKASDNVAPADRSATPATGSAITPATDGSVTPATDGSITPATDGSVTP	420
Db	361	GATSAEEDGAPAAAKASDNVAPADRSATPATGSAITPATDGSVTPATDGSITPATDGSVTP	420
Qy	421	VYDRSATPATDGSATPATIEESTVPTTQSSAMLATKAAATPEPMAQDSTAPESATQAP	480
Db	421	VYDRSATPATDGSATPATIEESTVPTTQSSAMLATKAAATPEPMAQDSTAPESATQAP	480
Qy	481	PSKSGEAAAGYAQESOREEAS 501	
Db	481	PSKSGEAAAGYAQESOREEAS 501	

```

RESULT 3
US-09-797-039-2
: Sequence 2, Application US/09797039
: Patent No. US20020042099A1
: GENERAL INFORMATION:
: APPLICANT: Olandt, Peter J.
: APPLICANT: Kapeller-Libermann, Rosana
: TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
: TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
: FILE REFERENCE: 10448-017001
: CURRENT APPLICATION NUMBER: US/09/797,039
: CURRENT FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: US 60/186,061
: PRIOR FILING DATE: 2000-02-29
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 501
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-797-039-2

```

Query Match	99.8%	Score 2577	DB 9	Length 501
Best Local Similarity	99.8%	Pred. No. 3.3e-160		
Matches 500; Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy	1	MPGCVTLDDKNVYNOPSEVTRVYLGAVI	KTEEECELFRAKDXTTKLHCKKFCRDG	60
Dp	1	MPGCVTLDDKNVYNOPSEVTRVYLGAVI	KTEEECELFRAKDXTTKLHCKKFCRDG	60
Qy	61	RKYRKAARKEIGILKMKVKNPILLOVDFEVT	REKEFFILELATGREVFDWILDDGYSSER	120
Dp	61	RKYRKAARKEIGILKMKVKNPILLOVDFEVT	REKEFFILELATGREVFDWILDDGYSSER	120
Qy	121	DTSNVTRQYVLEAVAYLHSLKI	VHRNLKLENTVYVNRLNKSKITVSDPHLAKL	ENGLIKEP 180
Dp	121	DTSNVTRQYVLEAVAYLHSLKI	VHRNLKLENTVYVNRLNKSKITVSDPHLAKL	ENGLIKEP 180
Qy	181	CGTPEYLAPEVTVGRQYRGYPVDCMAIGIM	YVILISGNPPEYEEVEEDDYASHNDKLFKFI	240
Dp	181	CGTPEYLAPEVTVGRQYRGYPVDCMAIGIM	YVILISGNPPEYEEVEEDDYASHNDKLFKFI	240
Qy	241	IADYDFEDSPYNDIDISQAAKDLVTLM	BEVDQRTAEALSHHWISGNAASDNINIDGV	3000
Dp	241	IADYDFEDSPYNDIDISQAAKDLVTLM	BEVDQRTAEALSHHWISGNAASDNINIDGV	3000
Qy	301	CAQIENKPFARKKKCAVRYTTLMKRLRA	PEOSTTAAASATATPAPGAAGATAAAS	3600
Dp	301	CAQIENKPFARKKKCAVRYTTLMKRLRA	PEOSTTAAASATATPAPGAAGATAAAS	3600
Qy	361	GATSAPEGDAAPAAASDNVAPADRSAT	PATDGSATPATDGSVTPATDGSITPATDGSVTP	4200
Dp	361	GATSAPEGDAAPAAASDNVAPADRSAT	PATDGSATPATDGSVTPATDGSITPATDGSVTP	4200

QY 421 VTRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
 Db 421 ATBRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
 QY 481 PSSKGEBAAGYAQESQREAS 501
 Db 481 PSSKGEBAAGYAQESQREAS 501

RESULT 4

US-10-423-543-19
 ; Sequence 19, Application US/10423543
 ; Publication No. US20040056355A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Libermann, Rosana K.
 ; APPLICANT: Hunter, John J.
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Olandt, Peter J.
 ; APPLICANT: Tsai, Fong-Ying
 ; APPLICANT: Galvin, Katherine M.
 ; APPLICANT: Chun, Myoung
 ; APPLICANT: Williams, Mark J.
 ; APPLICANT: Siles-Santiago, Inmaculada
 ; APPLICANT: Bandaru, Rajasekhar
 ; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
 ; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,
 ; TITLE OF INVENTION: 18610, 33217, 21967, 11983, 36555 OR 593 MOLECULES
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: MP103-0230ANIM
 ; CURRENT APPLICATION NUMBER: US/10/423,543
 ; PRIOR FILING DATE: 2003-04-25
 ; PRIOR APPLICATION NUMBER: US 10/278,036
 ; PRIOR FILING DATE: 2002-10-22
 ; PRIOR APPLICATION NUMBER: US 09/711,216
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: US 60/205,447
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 10/012,055
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/248,325
 ; PRIOR FILING DATE: 2000-11-14
 ; PRIOR APPLICATION NUMBER: US 10/003,690
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: US 60/248,893
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: US 09/797,039
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: US 60/186,061
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: US 10/217,168
 ; PRIOR FILING DATE: 2002-08-12
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 119
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 19
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-10-423-543-19

Query Match 99.8%, Score 2577, DB 12, Length 501,
 Best Local Similarity 99.8%, Pred. No. 3,3e-160,
 Matches 500, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 MPFGCVTLGDKKNTNQBSEVTDRLDGLQVTKTEFCETFPKADKTKTKTKTKCKKFGQRDS 60
 Db 1 MPFGCVTLGDKKNTNQBSEVTDRLDGLQVTKTEFCETFPKADKTKTKTKTKCKKFGQRDS 60
 QY 61 RKVKAAKNEIGILKMVGHPNLTQVDFVTRKEYTFLFELATGREVDMILDOGYSER 120

Db 61 RKVKAAKNEIGILKMVGHPNLTQVDFVTRKEYTFLFELATGREVDMILDOGYSER 120
 QY 121 DTSNVRQVLEAVNATLHSLKTVHRLKLENLVYNNRLKNSKIVSDFLATLGNLIEP 180
 Db 121 DTSNVRQVLEAVNATLHSLKTVHRLKLENLVYNNRLKNSKIVSDFLATLGNLIEP 180
 QY 181 CGTPEYLAPEVVGRORYGRPVDCAIGVITILSGNPFEEVEEDDYENHDKLFPKI 240
 Db 181 CGTPEYLAPEVVGRORYGRPVDCAIGVITILSGNPFEEVEEDDYENHDKLFPKI 240
 QY 241 IAGDYEFDSPYWDDISQAKDLVTRLMVEQDRTTEBAISHENISGNAASDKNIKGV 300
 Db 241 IAGDYEFDSPYWDDISQAKDLVTRLMVEQDRTTEBAISHENISGNAASDKNIKGV 300
 QY 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPESGSTRAPASATDTATGAGATPAAAS 360
 Db 301 CAQIEKNFAPAKKKAIVRTTLMKRLRAPESGSTRAPASATDTATGAGATPAAAS 360
 QY 361 GATSAPEGDAAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
 Db 361 GATSAPEGDAAAPAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
 QY 421 VTRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
 Db 421 ATBRSATPATDGRATPATEESTVPTTOSAMLATKAAATPEPMAAOPDSTAPEGATGQAP 480
 QY 481 PSSKGEBAAGYAQESQREAS 501
 Db 481 PSSKGEBAAGYAQESQREAS 501

RESULT 5

US-10-170-789-2
 ; Sequence 2, Application US/10170789
 ; Publication No. US20030180930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rachel E. Meyers
 ; APPLICANT: Olandt, Peter J.
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; APPLICANT: Curtis, Rory A. J.
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Welch, Nadine
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
 ; TITLE OF INVENTION: AND PROTEASE FAMILY MEMBERS AND USES THEREOF
 ; FILE REFERENCE: 10448-191001
 ; CURRENT APPLICATION NUMBER: US/10/170,789
 ; PRIOR FILING DATE: 2002-06-13
 ; PRIOR APPLICATION NUMBER: US 09/797,039
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/06525
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: US 60/186,061
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: US 09/882,166
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: PCT/US01/19269
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: US 60/212,078
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: US 09/934,406
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: PCT/US01/26052
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: US 60/226,740
 ; PRIOR FILING DATE: 2000-08-21
 ; PRIOR APPLICATION NUMBER: US 09/861,801
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: PCT/US01/16549
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: US 60/205,508
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 09/801,267
 ; PRIOR FILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: PCT/US01/07138
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/187,454
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/829,671
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: PCT/US01/40483
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,508
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/961,721
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: PCT/US01/29904
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/235,023
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US 10/045,367
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/246,561
PRIOR FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: US 09/801,275
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: PCT/US01/07074
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/187,420
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
US-10-170-789-2

Query Match 99.8%; Score 2577; DB 14; Length 501;
Best Local Similarity 99.8%; Pred. No. 3.3e-160;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPFGCVTLGDKKNYNPSEVTDRLDGVYKTEFCEIFRANKDTGKLTCKKFKRGD 60
DB 1 MPFGCVTLGDKKNYNPSEVTDRLDGVYKTEFCEIFRANKDTGKLTCKKFKRGD 60
QY 61 RKTKRKAANKIEIGILKWKHPNIIQLVDVFTYRKEVYIFLELATGRVFWILDQGYSSR 120
DB 61 RKTKRKAANKIEIGILKWKHPNIIQLVDVFTYRKEVYIFLELATGRVFWILDQGYSSR 120
QY 121 DTSNVVRQVLEAAVYHSLKIYHRNKLLENLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
DB 121 DTSNVVRQVLEAAVYHSLKIYHRNKLLENLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
QY 181 CGTPEYLAPEVVGROGRGVPCDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
DB 181 CGTPEYLAPEVVGROGRGVPCDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
QY 241 LAGDYFSDSPYWDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKGV 300
DB 241 LAGDYFSDSPYWDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKGV 300
QY 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSTAQAQASATDTATPPAAGATAAAS 360
DB 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSTAQAQASATDTATPPAAGATAAAS 360
QY 361 GATSAPEGDARAKSDNVAPADRATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 361 GATSAPEGDARAKSDNVAPADRATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
QY 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTPATDGSVTP 480
DB 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTPATDGSVTP 480
QY 481 PSSKGEBAAGYAOESQREAS 501
DB 481 PSSKGEBAAGYAOESQREAS 501

RESULT 6
US-10-085-198-6
Sequence 6, Application US/10085198
Publication No. US2004000907A1
GENERAL INFORMATION:
APPLICANT: Alabrock et al.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-279
CURRENT APPLICATION NUMBER: US/10/085,198
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/271,646
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/276,401
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/311,981
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/312,858
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/271,840
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/277,324
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/286,096
PRIOR FILING DATE: 2001-04-21
PRIOR APPLICATION NUMBER: 60/299,695
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 60/315,614
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/272,405
PRIOR FILING DATE: 2001-02-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 653
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 501
TYPE: PRT
ORGANISM: Homo sapiens
US-10-085-198-6

Query Match 99.8%; Score 2577; DB 15; Length 501;
Best Local Similarity 99.8%; Pred. No. 3.3e-160;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPFGCVTLGDKKNYNPSEVTDRLDGVYKTEFCEIFRANKDTGKLTCKKFKRGD 60
DB 1 MPFGCVTLGDKKNYNPSEVTDRLDGVYKTEFCEIFRANKDTGKLTCKKFKRGD 60
QY 61 RKTKRKAANKIEIGILKWKHPNIIQLVDVFTYRKEVYIFLELATGRVFWILDQGYSSR 120
DB 61 RKTKRKAANKIEIGILKWKHPNIIQLVDVFTYRKEVYIFLELATGRVFWILDQGYSSR 120
QY 121 DTSNVVRQVLEAAVYHSLKIYHRNKLLENLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
DB 121 DTSNVVRQVLEAAVYHSLKIYHRNKLLENLVYNNLKNKSKIVISDFHLAKLNGLIKEP 180
QY 181 CGTPEYLAPEVVGROGRGVPCDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
DB 181 CGTPEYLAPEVVGROGRGVPCDCAIGVIMYILSGNPFYEVEEDDYENHDKNLFKRI 240
QY 241 LAGDYFSDSPYWDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKGV 300
DB 241 LAGDYFSDSPYWDISQAADLVTRLMEVEQDORITAEBAISHEMIISGNAASDKNIKGV 300
QY 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSTAQAQASATDTATPPAAGATAAAS 360
DB 301 CAQIEKNFARAKKKAARVYTTLMKRLAPQSSTAQAQASATDTATPPAAGATAAAS 360
QY 361 GATSAPEGDARAKSDNVAPADRATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 361 GATSAPEGDARAKSDNVAPADRATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420

QY 421 VTDSATPATDGRATPATEESTVPTTQSSAMLATYAAATPEPAMAQPDSTAPEGATGQAP 480
 Db 421 ATDRSATPATDGRATPATEESTVPTTQSSAMLATYAAATPEPAMAQPDSTAPEGATGQAP 480
 QY 481 PSSKGEAAGYAQESQREAS 501
 Db 481 PSSKGEAAGYAQESQREAS 501

RESULT 7 US-10-258-106-17

; Sequence 17, Application US/10258106
 ; Publication No. US20040018185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
 ; APPLICANT: GANDHI, Ameena R.; TRIBOULEY, Catherine M.
 ; APPLICANT: KEARNEY, Liam; GRIFFIN, Jennifer A.
 ; APPLICANT: NGUYEN, Daniel B.; BANDMAN, Olga
 ; APPLICANT: LU, Dying Aina M.; LAU, Preeti G.
 ; APPLICANT: BURFORD, Neil; KHAN, Farrah A.
 ; APPLICANT: WALIA, Narinder K.; YAO, Monique G.
 ; APPLICANT: MARCUS, Gregory A.; BURRILL, John D.
 ; APPLICANT: PATTERSON, Chandra; ZINGLER, Kurt A.
 ; APPLICANT: RECIPON, Shirley A.; LU, Yan
 ; APPLICANT: TANG, Y. Tom; HAFALIA, April J.A.
 ; APPLICANT: ELIOT, Vicki S.; BAUGHN, Mariah R.
 ; APPLICANT: WALSH, Roderick T.; RAMKOMAR, Jayalaxmi
 ; APPLICANT: BOROWSKY, Mark L.; AU-YOUNG, Janice K.
 ; APPLICANT: HILLMAN, Jennifer L.; GURUPAJAN, Rajagopal
 ; TITLE OF INVENTION: HUMAN KINASES
 ; FILE REFERENCE: PI-0076 USN
 ; CURRENT APPLICATION NUMBER: US/10/258, 106
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: PCT/US01/12392
 ; PRIOR FILING DATE: 2001-04-20
 ; PRIOR APPLICATION NUMBER: US 60/199, 021
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/200, 226
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: US 60/202, 339
 ; PRIOR FILING DATE: 2000-05-05
 ; PRIOR APPLICATION NUMBER: US 60/203, 505
 ; PRIOR FILING DATE: 2000-05-11
 ; PRIOR APPLICATION NUMBER: US 60/205, 654
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 60/207, 739
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/208, 795
 ; PRIOR FILING DATE: 2000-06-01
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 17
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20040018185A1 71584520CD1
 ; US-10-258-106-17

Query Match 99.8%; Score 2577; DB 15; Length 501;
 Best Local Similarity 99.8%; Pred. No. 3.3e-160;
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPFGCVTLGSKKNYNQSEVYTDRLDGLGVITKEEFCIFPAKDKTTGKLTCKKFKQKDG 60
 Db 1 MPFGCVTLGSKKNYNQSEVYTDRLDGLGVITKEEFCIFPAKDKTTGKLTCKKFKQKDG 60
 QY 61 RKVRKAANKNEIGILKMKVHPNIIQLVDVFTVRKEYFFLELATGREVFWILDGYYSER 120
 Db 61 RKVRKAANKNEIGILKMKVHPNIIQLVDVFTVRKEYFFLELATGREVFWILDGYYSER 120

QY 121 DTSNVVROVLBAVAYLHSLKIVHRNLKLENTLYVYRNLKSKIVISDFHLAKLENGLIKPEP 180
 Db 121 DTSNVVROVLBAVAYLHSLKIVHRNLKLENTLYVYRNLKSKIVISDFHLAKLENGLIKPEP 180
 QY 181 CGTPEYLAPEVVGQRQYGRPVDCWAIQVIMYILLSGNPFYEVEEDDYENHDKLFRKI 240
 Db 181 CGTPEYLAPEVVGQRQYGRPVDCWAIQVIMYILLSGNPFYEVEEDDYENHDKLFRKI 240
 QY 241 LAGDYEFDSPYWDDISQAQKDLVTRLMVEYQDQRTAEALISHEWISGAADKXIKQCV 300
 Db 241 LAGDYEFDSPYWDDISQAQKDLVTRLMVEYQDQRTAEALISHEWISGAADKXIKQCV 300
 QY 301 CAQIEGNFPAKMKKAVRTTLMKRLRABEGSSTAAQASATDTPATPAGATPAAAS 360
 Db 301 CAQIEGNFPAKMKKAVRTTLMKRLRABEGSSTAAQASATDTPATPAGATPAAAS 360
 QY 361 GATSAPBGPABAAKSDNVAAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 Db 361 GATSAPBGPABAAKSDNVAAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 QY 421 VTDSATPATDGRATPATEESTVPTTQSSAMLATYAAATPEPAMAQPDSTAPEGATGQAP 480
 Db 421 ATDRSATPATDGRATPATEESTVPTTQSSAMLATYAAATPEPAMAQPDSTAPEGATGQAP 480
 QY 481 PSSKGEAAGYAQESQREAS 501
 Db 481 PSSKGEAAGYAQESQREAS 501

RESULT 8 US-10-425-114-54473

; Sequence 34473, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingsong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425, 114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 54473
 ; LENGTH: 473
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB4654-060-E3_FLI.pep
 ; US-10-425-114-54473

Query Match 93.1%; Score 2402.5; DB 12; Length 473;
 Best Local Similarity 93.6%; Pred. No. 7.6e-149;
 Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

QY 1 MPFGCVTLGDKKNYNQSEVYTDRLDGLGVITKEEFCIFPAKDKTTGKLTCKKFKQKDG 60
 Db 4 MPFGCVTLGDKKNYNQSEVYTDRLDGLGVITKEEFCIFPAKDKTTGKLTCKKFKQKDG 63
 QY 61 RKVRKAANKNEIGILKMKVHPNIIQLVDVFTVRKEYFFLELATGREVFWILDGYYSER 120
 Db 64 RKVRKAANKNEIGILKMKVHPNIIQLVDVFTVRKEYFFLELATGREVFWILDGYYSER 123
 QY 121 DTSNVVROVLBAVAYLHSLKIVHRNLKLENTLYVYRNLKSKIVISDFHLAKLENGLIKPEP 180
 Db 124 DTSNVVROVLBAVAYLHSLKIVHRNLKLENTLYVYRNLKSKIVISDFHLAKLENGLIKPEP 183
 QY 181 CGTPEYLAPEVVGQRQYGRPVDCWAIQVIMYILLSGNPFYEVEEDDYENHDKLFRKI 240
 Db 184 CGTPEYLAPEVVGQRQYGRPVDCWAIQVIMYILLSGNPFYEVEEDDYENHDKLFRKI 243

QY 241 LAGDYEFDSPPYMDDISQAADLVTRIMEVEODORTIAEBAISHEMI SGNAASDKNIXGV 300
DB 244 LAGDYEFDSPPYMDDISQAADLVTRIMEVEODORTIAEBAISHEMI SGNAASDKNIXGV 303
QY 301 CAQIEKNFAPAAKKKAVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 360
DB 304 CAQIEKNFAPAAKKKAVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 353
QY 361 GATSABEGDAPAAKSDNVAADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 354 -----ADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 392
QY 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 480
DB 393 ATDRSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 452
QY 481 PSSKGEBAAGYAQESQREAS 501
DB 453 PSSKGEBAAGYAQESQREAS 473

RESULT 9
US-10-425-114-54513

; Sequence 54513, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54513
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4654-022-E3_F11.pcp
US-10-425-114-54513

Query Match 93.1%; Score 2402.5; DB 12; Length 473;
Best Local Similarity 93.6%; Pred. No. 7.6e-149;
Matches 469; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

QY 1 MPFGCTTLDGKKNYNSPSEVTDRYDGOVITKEFEIRADKTTGKHTKKQKDG 60
DB 4 MPFGCTTLDGKKNYNSPSEVTDRYDGOVITKEFEIRADKTTGKHTKKQKDG 63
QY 61 RKYRKAAXKEIGILKNVKNPNILQVDVETVTRKEYTIFELATGSEVPMILDDGYYSR 120
DB 64 RKYRKAAXKEIGILKNVKNPNILQVDVETVTRKEYTIFELATGSEVPMILDDGYYSR 123
QY 121 DTSNVVROYLVAAYLHSLKIVHRNLKLENLVYNNLKNKSKIVISDFHLAKLENGLIKPEP 180
DB 124 DTSNVVROYLVAAYLHSLKIVHRNLKLENLVYNNLKNKSKIVISDFHLAKLENGLIKPEP 183
QY 181 CGTPEYLAEBVGRQYGRPVDCWALGVIMYILLSGNPPFYEEVEDDYENHDKULFRKI 240
DB 184 CGTPEYLAEBVGRQYGRPVDCWALGVIMYILLSGNPPFYEEVEDDYENHDKULFRKI 243
QY 241 LAGDYEFDSPPYMDDISQAADLVTRIMEVEODORTIAEBAISHEMI SGNAASDKNIXGV 300
DB 244 LAGDYEFDSPPYMDDISQAADLVTRIMEVEODORTIAEBAISHEMI SGNAASDKNIXGV 303
QY 301 CAQIEKNFAPAAKKKAVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 360

DB 304 CAQIEKNFAPAAKKKAVRTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAAS 353
QY 361 GATSABEGDAPAAKSDNVAADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 420
DB 354 -----ADRSATPATDGSATPATDGSVTPATDGSITPATDGSVTP 392
QY 421 VTRDSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 480
DB 393 ATDRSATPATDGSATPATDGSITPATDGSVTPATDGSITPATDGSVTP 452
QY 481 PSSKGEBAAGYAQESQREAS 501
DB 453 PSSKGEBAAGYAQESQREAS 473

RESULT 10
US-10-425-114-54471

; Sequence 54471, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54471
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4676-058-A2_F11.pcp
US-10-425-114-54471

Query Match 56.8%; Score 1457.5; DB 12; Length 317;
Best Local Similarity 94.8%; Pred. No. 2.4e-87;
Matches 291; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 196 RYGRPVDCWALGVIM-YILLSGNPPFYEEVEDDYENHDKULFRKTLAGDYEFDSPPYMD 254
DB 11 RYGRPVDCWALGVIM-YILLSGNPPFYEEVEDDYENHDKULFRKTLAGDYEFDSPPYMD 70
QY 255 ISQAADLVTRIMEVEODORTIAEBAISHEMI SGNAASDKNIXGVCAQIEKNFAPAAKK 314
DB 71 ISQAADLVTRIMEVEODORTIAEBAISHEMI SGNAASDKNIXGVCAQIEKNFAPAAKK 130
QY 315 KAVVTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAASGATAPBEGDAPAA 374
DB 131 KAVVTTLMKRLAPBQSSSTAQAASATDPATPGAGATAAASGATAPBEGDAPAA 190
QY 375 KSDNVAPADRSATPATDGSATPATDGSITPATDGSITPATDGSVTPVTRDSATPATDGRA 434
DB 191 KSDNVAPADRSATPATDGSATPATDGSITPATDGSITPATDGSVTPVTRDSATPATDGRA 250
QY 435 TPATBESVTPPTQSSAMLATKAAATPEPMAOPDSTAPBEGATQAPSSKGEBAAGYAQ 494
DB 251 TPATBESVTPPTQSSAMLATKAAATPEPMAOPDSTAPBEGATQAPSSKGEBAAGYAQ 310
QY 495 SORREAS 501
DB 311 SORREAS 317

RESULT 11
US-09-764-875-725
; Sequence 725, Application US/09764875
; Publication No. US20040018969A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P202
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 725
LENGTH: 204
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (197)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-725

Query Match 37.4%; Score 966; DB 11; Length 204;
Best Local Similarity 98.4%; Pred. No. 1.8e-55;
Matches 187; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 186 YLAEVVGQRGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 245
14 FVAPEVVGQRGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 73
QY 246 EFDSPLYMDISQAADLVTRLMVEVQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 305
74 EFDSPLYMDISQAADLVTRLMVEVQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 133
Db 306 KNFARAKKKAVRVTTLMKRLRAPEQSSSTAAGSATDTATPGAGGATAAASGATSA 365
134 KNFARAKKKAVRVTTLMKRLRAPEQSSSTAAGSATDTATPGAGGATAAASGATSA 193
QY 366 PEGDAARAASD 375
Db 194 PEGDAARAASD 203

RESULT 12
US-09-764-868-832
Sequence 832, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P202
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 832
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (74)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (162)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-832

Query Match 33.0%; Score 852; DB 9; Length 219;

Best Local Similarity 72.6%; Pred. No. 5.4e-48;
Matches 172; Conservative 5; Mismatches 20; Indels 40; Gaps 2;
QY 186 YLAEVVGQRGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 245
14 FVAPEVVGQRGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 73
QY 246 EFDSPLYMDISQAADLVTRLMVEVQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 305
74 EFDSPLYMDISQAADLVTRLMVEVQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 133
Db 306 KNFARAKKKAVRVTTLMKRLRAPEQSSSTAAGSATDTATPGAGGATAAASGATSA 365
134 KNFARAKKKAVRVTTLMKRLRAPEQSSSTAAGSATDTATPGAGGATAAASGATSA 178
QY 366 PEGDAARAASD 375
Db 179 PEGDAARAASD 203

RESULT 13
US-09-764-875-1035
Sequence 1035, Application US/09764875
Patent No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P202
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1035
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (74)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (162)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-1035

Query Match 33.0%; Score 852; DB 11; Length 219;
Best Local Similarity 72.6%; Pred. No. 5.4e-48;
Matches 172; Conservative 5; Mismatches 20; Indels 40; Gaps 2;

QY 186 YLAEVVGQRGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 245
14 FVAPEVVGQRGRYGRVDCMAIGVIMYLLSGNPPFYEEVEDDYENHDKLFRKILAGDY 73
QY 246 EFDSPLYMDISQAADLVTRLMVEVQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 305
74 EFDSPLYMDISQAADLVTRLMVEVQDQRTAEBAISHEMIISGNAASDKNIKDVCAQIE 133
Db 306 KNFARAKKKAVRVTTLMKRLRAPEQSSSTAAGSATDTATPGAGGATAAASGATSA 365
134 KNFARAKKKAVRVTTLMKRLRAPEQSSSTAAGSATDTATPGAGGATAAASGATSA 178
QY 366 PEGDAARAASD 375
Db 179 PEGDAARAASD 203

RESULT 14
US-09-817-181-4
Sequence 4, Application US/09817181
Patent No. US20020142427A1
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C1001189
CURRENT APPLICATION NUMBER: US/09/817,181
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 370
TYPE: PRS
ORGANISM: Human
US-09-817-181-4

Query Match 30.7%; Score 793; DB 9; Length 370;
Best Local Similarity 43.7%; Pred. No. 7, 4e-44;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;

14 YNPSSEVTDYDVGQYKTEEFCEIFRAKDXTGKLTCKKFKRGRKRAKNEIGI 73
10 WKQAEIDRIDYDFRDVLTGAFSEVILAEKRTQKVAIKIAKEALBEGKSGMENEIAY 69
74 LKQVGHENILQVDVFNTRKEVFIPLATGREVPMIDOGYSEBRTSNVRYOLEAV 133
70 LKIKHPNIVALLDDYESGHLTYLMQVSGELFRIYKGFYTERASRLIFQVLDAY 129
134 AYLSLKIYVRNKLKENTLVYVNRKLSKIIVSDPHLAKLEN--GLIKPCGTPBYLAPEV 191
130 KILHDLGIYVRDLKPENLIIYSLDEDSKIMISDFGLSKNEDPGSVLSTACGTGVAPEV 189
192 VGRQRYRPVDCVAIGVIMYILLSGNPPFYEEVEDDYENHDKNLFKRIIAGDYEPDSPY 251
190 LQKPYSKAVDCWSIGIVAYIILCGYPPFYDE-----NDAKLFEQILKAEYEPDSPY 241
252 WDDISQAADLVTRIMEVEODQRTAEALSHWISGNAASDKNTKDGVCAGIENKPARA 311
242 WDDISQADLVTRIMEVEODQRTAEALSHWISGNAASDKNTKDGVCAGIENKPARA 311
312 KMKKAVRVTTLMKRLAPE--QSTAAQASASATDTPGAGGATAAASGATSAP 366
302 KMKQAFNATVAVRMKRLQLTGTSQEGQGTASHGELLTPVAGGPAAGCCCRDCCVP 358

RESULT 15
US-09-769-970-19
Sequence 19, Application US/09769970
Publication No. US20030170219A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Corley, Neil G.
Guegler, Karl G.
Lal, Preeti
Goli, Surya K.
Shah, Puri
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,970
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/272,796
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 790790
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-769-970-19

Query Match 30.7%; Score 793; DB 10; Length 370;
Best Local Similarity 43.7%; Pred. No. 7, 4e-44;
Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;
14 YNPSSEVTDYDVGQYKTEEFCEIFRAKDXTGKLTCKKFKRGRKRAKNEIGI 73
10 WKQAEIDRIDYDFRDVLTGAFSEVILAEKRTQKVAIKIAKEALBEGKSGMENEIAY 69
74 LKQVGHENILQVDVFNTRKEVFIPLATGREVPMIDOGYSEBRTSNVRYOLEAV 133
70 LKIKHPNIVALLDDYESGHLTYLMQVSGELFRIYKGFYTERASRLIFQVLDAY 129
134 AYLSLKIYVRNKLKENTLVYVNRKLSKIIVSDPHLAKLEN--GLIKPCGTPBYLAPEV 191
130 KILHDLGIYVRDLKPENLIIYSLDEDSKIMISDFGLSKNEDPGSVLSTACGTGVAPEV 189
192 VGRQRYRPVDCVAIGVIMYILLSGNPPFYEEVEDDYENHDKNLFKRIIAGDYEPDSPY 251
190 LQKPYSKAVDCWSIGIVAYIILCGYPPFYDE-----NDAKLFEQILKAEYEPDSPY 241
252 WDDISQAADLVTRIMEVEODQRTAEALSHWISGNAASDKNTKDGVCAGIENKPARA 311
242 WDDISQADLVTRIMEVEODQRTAEALSHWISGNAASDKNTKDGVCAGIENKPARA 311
312 KMKKAVRVTTLMKRLAPE--QSTAAQASASATDTPGAGGATAAASGATSAP 366
302 KMKQAFNATVAVRMKRLQLTGTSQEGQGTASHGELLTPVAGGPAAGCCCRDCCVP 358

Search completed: April 23, 2004, 15:55:38
Job time : 50 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:47:09 ; Search time 23 Seconds

(without alignments)
1124.548 Million cell updates/sec

Title: US-10-669-689-2

Perfect score: 2581

Sequence: 1 MPFGCVTLGDKKNVQPSSEV.....SSKGEFAGYAGSOREAS 501

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2581	100.0	501	US-09-734-030-2	Sequence 2, Appl1
2	2581	100.0	501	US-10-153-921-2	Sequence 2, Appl1
3	793	30.7	370	US-08-878-989-19	Sequence 19, Appl1
4	793	30.7	370	US-09-272-796-19	Sequence 19, Appl1
5	793	30.7	370	US-09-457-0408-31	Sequence 31, Appl1
6	767.5	29.7	385	US-09-733-388-2	Sequence 2, Appl1
7	764	29.6	355	US-09-579-664B-10	Sequence 10, Appl1
8	754.5	29.2	356	US-09-733-388-4	Sequence 4, Appl1
9	715	27.7	358	US-09-230-896C-29	Sequence 4, Appl1
10	642.5	24.9	343	US-08-878-989-5	Sequence 5, Appl1
11	642.5	24.9	343	US-09-272-796-5	Sequence 5, Appl1
12	589.5	22.8	424	US-08-715-568A-1	Sequence 1, Appl1
13	580.5	22.5	765	US-09-975-326-4	Sequence 4, Appl1
14	580.5	22.5	765	US-10-217-357-4	Sequence 4, Appl1
15	580.5	22.5	766	US-09-975-326-2	Sequence 2, Appl1
16	580.5	22.5	766	US-10-217-357-2	Sequence 2, Appl1
17	565.5	21.9	565	US-09-800-960-2	Sequence 2, Appl1
18	565.5	21.9	565	US-10-096-960-2	Sequence 2, Appl1
19	546	21.2	566	US-07-857-224B-24	Sequence 24, Appl1
20	535	20.7	556	US-09-800-960-4	Sequence 4, Appl1
21	535	20.7	556	US-10-096-960-4	Sequence 4, Appl1
22	504	19.5	264	US-07-857-224B-18	Sequence 18, Appl1
23	490	19.0	264	US-07-857-224B-19	Sequence 19, Appl1
24	489.5	19.0	295	US-07-951-715A-23	Sequence 23, Appl1
25	489.5	19.0	295	US-08-459-448A-23	Sequence 23, Appl1
26	489.5	19.0	295	US-08-459-595A-23	Sequence 23, Appl1
27	489.5	19.0	295	US-08-459-504B-23	Sequence 23, Appl1

28	489.5	19.0	295	US-08-459-444-23	Sequence 23, Appl1
29	489.5	19.0	295	US-09-547-422-23	Sequence 23, Appl1
30	483.5	18.7	331	US-08-810-712-24	Sequence 24, Appl1
31	483.5	18.7	1423	US-08-810-712-10	Sequence 10, Appl1
32	480.5	18.6	514	US-09-841-683-2	Sequence 2, Appl1
33	468.5	18.2	817	US-09-992-481-4	Sequence 4, Appl1
34	467	18.1	387	US-08-713-828-3	Sequence 3, Appl1
35	467	18.1	387	US-08-919-627-3	Sequence 3, Appl1
36	467	18.1	387	US-09-096-245-3	Sequence 3, Appl1
37	467	18.1	387	US-09-457-040B-30	Sequence 30, Appl1
38	460	17.8	454	US-09-159-385-1	Sequence 1, Appl1
39	460	17.8	454	US-09-186-277-1	Sequence 1, Appl1
40	459.5	17.8	388	US-08-713-828-5	Sequence 5, Appl1
41	459.5	17.8	388	US-08-919-627-5	Sequence 5, Appl1
42	459.5	17.8	388	US-09-096-245-5	Sequence 5, Appl1
43	457	17.7	388	US-08-713-828-4	Sequence 4, Appl1
44	457	17.7	388	US-08-919-627-4	Sequence 4, Appl1
45	457	17.7	388	US-09-096-245-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1				
US-09-734-030-2				
Sequence 2, Application US/09734030				
Patent No. 6461846				
GENERAL INFORMATION:				
APPLICANT: BEASLEY, Ellen M.				
APPLICANT: MERKLOV, Gennady				
APPLICANT: KETCHUM, Karen A.				
APPLICANT: WEI, Ming-Hui				
APPLICANT: DIPRANCESCO, Valentina				
APPLICANT: YAN, Chunhua				
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC				
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES				
TITLE OF INVENTION: THERMOF				
FILE REFERENCE: CLO00612				
CURRENT APPLICATION NUMBER: US/09/734,030				
CURRENT FILING DATE: 2000-12-12				
PRIOR APPLICATION NUMBER: 60/207,261				
PRIOR FILING DATE: 2000-05-30				
NUMBER OF SEQ ID NOS: 3				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 2				
LENGTH: 501				
TYPE: PRT				
ORGANISM: HUMAN				
US-09-734-030-2				
Query Match				
Best Local Similarity 100.0%; Pred. No. 4.1e-160; Length 501,				
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MPFGCVTLGDKKNVQPSSEVTRDYDLGVIKTEBCEIFRAKDKTGTGKATCKFKQKDG	60	
DB	1	MPFGCVTLGDKKNVQPSSEVTRDYDLGVIKTEBCEIFRAKDKTGTGKATCKFKQKDG	60	
QY	61	RKVRKAANEIGILKVNKHPNLIQVDFVTRKEYFIFLELATGREVFDMIDQYSEER	120	
DB	61	RKVRKAANEIGILKVNKHPNLIQVDFVTRKEYFIFLELATGREVFDMIDQYSEER	120	
QY	121	DSNVNRYQTELVAVLHSLIKYHRLKLENNVYVYRLKNSKIVISDFHLAKLENLKEP	180	
DB	121	DSNVNRYQTELVAVLHSLIKYHRLKLENNVYVYRLKNSKIVISDFHLAKLENLKEP	180	
QY	181	CGPEYLAPEVVGRRYGRPVDCMAIGVIMYILSGNPFYEVEEDYENHDKLFRKI	240	
DB	181	CGPEYLAPEVVGRRYGRPVDCMAIGVIMYILSGNPFYEVEEDYENHDKLFRKI	240	
QY	241	LAGDYEFDSPYWDDISQAKDLYVTLMEVEQDRIITAEASISHEWISGNMAASDKNIKDGV	300	
DB	241	LAGDYEFDSPYWDDISQAKDLYVTLMEVEQDRIITAEASISHEWISGNMAASDKNIKDGV	300	

Qy	30	CAIEENGPAPAKKKKAVVYITLMKSLRPBEGSSTAAAGSAATPTAPGAAGAATAAAS	360
Db	301	CAOIEGNPAPAKKKKAVVYITLMKSLRPBEGSSTAAAGSATUTATPGANGATAAAS	360
Qy	361	GATSAEEDGAPAAAKSDNVAPADRSTATPDGSATPATDGSVTPTDGSITTPATDGSVTP	420
Db	361	GATSAEEDGAPAAAKSDNVAPADRSTATPDGSATPATDGSVTPTDGSITTPATDGSVTP	420
Qy	421	VTRSRATPATDGHATPATTEESTVPTTOSAMLATGAATPEPPAMAOPDSTAPEGATGOAF	480
Db	421	VTRSRATPATDGHATPATTEESTVPTTOSAMLATGAATPEPPAAPDPSTAPEGATGOAF	480
Qy	481	PSSKGEEAAGVAOESOREEAS	501
Db	481	PSSKGEEAAGVAOESOREEAS	501

```

RESULT 2
US-10-153-921-2
/ Sequence 2, Application US/10153921
/ Patent No. 665316
/ GENERAL INFORMATION:
/ APPLICANT: YAN, Chunhua et al.
/ TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
/ TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: CLO006122D1V
/ CURRENT APPLICATION NUMBER: US/10/153,921
/ CURRENT FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: 60/207,281
/ PRIOR FILING DATE: 2000-05-30
/ PRIOR APPLICATION NUMBER: 09/734,030
/ PRIOR FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 501
/ TYPE: PRT
/ ORGANISM: HOMO SAPIEN
US-10-153-921-2

```

Query Match	100.0%;	Score 2581;	DB 4;	Length 501;
Best Local Similarity	100.0%;	Pred. No. 4.1e-180;		
Matches 501; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	MPGCVTLDDKKNYNQPSVETVRYLQGVKITKEECE:FRAXDXTTKGKTKCKKPKQRO	60
Dp	1	MPGCVTLDDKKNYNQPSVETVRYLQGVKITKEECE:FRAXDXTTKGKTKCKKPKQRO	60
QY	61	RKYRKAAXNEIGILKMKVKKHPIILQVDVFVTRKEVFLELATGREVFWDILDOGYSSER	120
Dp	61	RKYRKAAXNEIGILKMKVKKHPIILQVDVFVTRKEVFLELATGREVFWDILDOGYSSER	120
QY	121	DTSNVVRQVLEAVAYIHSIKIVHRUKLENIYYTRKLNKSTIVSDPHLAKLENGLIKKEP	180
Dp	121	DTSNVVRQVLEAVAYIHSIKIVHRUKLENIYYTRKLNKSTIVSDPHLAKLENGLIKKEP	180
QY	181	CGSEVTLAPEVNGROGYSRPVDCMALGIYIMTILISGNPFEEVEEDYENHDKN:PRKI	240
Dp	181	CGSEVTLAPEVNGROGYSRPVDCMALGIYIMTILISGNPFEEVEEDYENHDKN:PRKI	240
QY	241	IAGDYEFDSPPYDDDISQAADLVTRILMEVQDQRTAEALSHWISIGNAASDKNIKDYV	300
Dp	241	IAGDYEFDSPPYDDDISQAADLVTRILMEVQDQRTAEALSHWISIGNAASDKNIKDYV	300
QY	301	CAQIEKNFPAKWKKAIVRTTLMKELRAPESOSTPAASASATDTATPAGAGATAAAS	360
Dp	301	CAQIEKNFPAKWKKAIVRTTLMKELRAPESOSTPAASASATDTATPAGAGATAAAS	360
QY	361	GATSAPEGGAAPAAASDNVAPADRBRATATGSAIPATDGSVTATDGSITPATDGSVTP	420
Dp	361	GATSAPEGGAAPAAASDNVAPADRBRATATGSAIPATDGSVTATDGSITPATDGSVTP	420

Qy	Db	Qy	Db
422	VYDRSASTPTDGRAPATPEESTVPTOSAAATLAKAATPEPAAQDPSTAPGATGQAP	481	PSKSGEAAAGYAOESQREZAS 501
421	VYDRSASTPTDGRAPATPEESTVPTOSAAATLAKAATPEPAAQDPSTAPGATGQAP	481	PSKSGEAAAGYAOESQREZAS 501

RESULT 3
US-08-878-989-19
; Sequence 19, Application US/08878989

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Guegler, Karl G.

APPLICANT: Goli, Surya K

TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

NUMBER OF SEQUENCES: 21

ADDRESSEE: Incyte Pharmaceuticals, Inc.

CITY: Palo Alto

COUNTRY: USA

COMPUTER READAB ;

COMPUTER: IBM compatible

```
SOFTWARE: FastSeq for W1
```

APPLICATION NUMBER: US/0

CLASSIFICATION: 435

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION ;

TELEFAX: 415-845-4100

INFORMATION FOR SEQ ID NO

LENGTH: 370 amino acids

STRANDEDNESS: single

IMMEDIATE SOURCE:

CLONE: 790790

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Best Local Similarity	43
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[illegible][illegible]

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7 DECEMBER 1997

[illegible]

Db 70 LHKIKHPNIVALDDIYESSGSHLYLMQVSGGELFDRIVEKGYTERDASRLIFQVLDAY 129
 QY 134 AYHSLKTVHRLKLENTVYNNRLKNSKIVISDFHLAKLEN--GLIKEPGCTPEYLAPEV 191
 Db 130 KYLHDLGIYHRDLKLENLLYSLEDSKIMISDFGLSKNEPDSGLSTACGTPGVAPAEV 189
 QY 192 VGRQYGRPVDCMAIGVIMYILLSGNPFEEVEEDDYENHDKLFRKILLAGDYFDSPY 251
 Db 190 LAQKPYSAKVDGWSIGVIAIYLLCGYPPFYDE-----NDAKLFEQILKAIEYFDSPY 241
 QY 252 WDISQAADLVTRLMEVEODORTAEALISHEMISGNAASDKNIKDGVCAGQIEKNFARA 311
 Db 242 WDISDAKDFIRHLMKEDPEKRTCEQALQHPWLAGDTALDKNIHQSVSEQIKKNFAKS 301
 QY 312 KWKAQAVRTTLMKRLRAPE--QSTTAAQASATDTATPGAGATATAAASGATSAP 366
 Db 302 KWKAQAFNATAVVRHMRKLQIGTSGEGGQTASHGELLTPVAGGPAGCCCRDCCVER 358

RESULT 4
 US-09-272-796-19
 ; Sequence 19, Application US/09272796
 ; Patent No. 6207148
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl G.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Shah, Purya
 ; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 ; TITLE OF INVENTION: KINASES
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: PaeSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/272,796
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/878,989
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0321 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 370 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 790790
 ; US-09-272-796-19

Query Match 30.7%, Score 793, DB 3, Length 370;

Best Local Similarity 43.7%, Pred. No. 4.3e-50;
 Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;

QY 14 YNPSVETDRYDLGVITKEEFCIFRAKDTTKGLTKCKFRQDRGKVRKAAKEIGI 73
 Db 10 WKQADIRIDYDFRDVLGTGAFSEVILAEDEKRTQKVAIKIAEALGEGKSENEIAY 69
 QY 74 LKMKVHNILQVDFVTRKEVIFLELATGREVDWLLDGGYSEEDTSNVVRQVLEAV 133
 Db 70 LHKIKHPNIVALDDIYESSGSHLYLMQVSGGELFDRIVEKGYTERDASRLIFQVLDAY 129
 QY 134 AYHSLKTVHRLKLENTVYNNRLKNSKIVISDFHLAKLEN--GLIKEPGCTPEYLAPEV 191
 Db 130 KYLHDLGIYHRDLKLENLLYSLEDSKIMISDFGLSKNEPDSGLSTACGTPGVAPAEV 189
 QY 192 VGRQYGRPVDCMAIGVIMYILLSGNPFEEVEEDDYENHDKLFRKILLAGDYFDSPY 251
 Db 190 LAQKPYSAKVDGWSIGVIAIYLLCGYPPFYDE-----NDAKLFEQILKAIEYFDSPY 241
 QY 252 WDISQAADLVTRLMEVEODORTAEALISHEMISGNAASDKNIKDGVCAGQIEKNFARA 311
 Db 242 WDISDAKDFIRHLMKEDPEKRTCEQALQHPWLAGDTALDKNIHQSVSEQIKKNFAKS 301
 QY 312 KWKAQAVRTTLMKRLRAPE--QSTTAAQASATDTATPGAGATATAAASGATSAP 366
 Db 302 KWKAQAFNATAVVRHMRKLQIGTSGEGGQTASHGELLTPVAGGPAGCCCRDCCVER 358

RESULT 5
 US-09-457-040B-31
 ; Sequence 31, Application US/09457040B
 ; Patent No. 6387641
 ; GENERAL INFORMATION:
 ; APPLICANT: Vertex Pharmaceuticals Incorporated
 ; APPLICANT: Bellon, Steve
 ; TITLE OF INVENTION: Crystallized P38 Complexes
 ; FILE REFERENCE: VPI/98-14
 ; CURRENT APPLICATION NUMBER: US/09/457,040B
 ; CURRENT FILING DATE: 1999-12-08
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-457-040B-31

Query Match 30.7%, Score 793, DB 4; Length 370;
 Best Local Similarity 43.7%, Pred. No. 4.3e-50;
 Matches 156; Conservative 69; Mismatches 120; Indels 12; Gaps 3;

QY 14 YNPSVETDRYDLGVITKEEFCIFRAKDTTKGLTKCKFRQDRGKVRKAAKEIGI 73
 Db 10 WKQADIRIDYDFRDVLGTGAFSEVILAEDEKRTQKVAIKIAEALGEGKSENEIAY 69
 QY 74 LKMKVHNILQVDFVTRKEVIFLELATGREVDWLLDGGYSEEDTSNVVRQVLEAV 133
 Db 70 LHKIKHPNIVALDDIYESSGSHLYLMQVSGGELFDRIVEKGYTERDASRLIFQVLDAY 129
 QY 134 AYHSLKTVHRLKLENTVYNNRLKNSKIVISDFHLAKLEN--GLIKEPGCTPEYLAPEV 191
 Db 130 KYLHDLGIYHRDLKLENLLYSLEDSKIMISDFGLSKNEPDSGLSTACGTPGVAPAEV 189
 QY 192 VGRQYGRPVDCMAIGVIMYILLSGNPFEEVEEDDYENHDKLFRKILLAGDYFDSPY 251
 Db 190 LAQKPYSAKVDGWSIGVIAIYLLCGYPPFYDE-----NDAKLFEQILKAIEYFDSPY 241
 QY 252 WDISQAADLVTRLMEVEODORTAEALISHEMISGNAASDKNIKDGVCAGQIEKNFARA 311
 Db 242 WDISDAKDFIRHLMKEDPEKRTCEQALQHPWLAGDTALDKNIHQSVSEQIKKNFAKS 301
 QY 312 KWKAQAVRTTLMKRLRAPE--QSTTAAQASATDTATPGAGATATAAASGATSAP 366

Db 302 KKQAFNATAVVRHNRKQLGTSQSGOGTASHGSHLLTPVAGGPAAGCCCDCCVP 356

RESULT 6
US-09-733-388-2
Sequence 2, Application US/09733388

Patent No. 6602698
GENERAL INFORMATION:
APPLICANT: Donoho, Greg
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Abulin, Alejandro
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/09/733,388
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 385
TYPE: PRT
ORGANISM: Homo sapiens
US-09-733-388-2

Query Match 29.7%; Score 767.5; DB 4; Length 385;
Best Local Similarity 40.4%; Pred. No. 3.3e-48;
Matches 152; Conservative 79; Mismatches 122; Indels 23; Gaps 5;

QY 16 QPSEVTDRYDLGVITKEEFCEIFRAKDKTTGKLTCKKFKQKDRGRKRAKANEIGILK 75
DB 15 QADIDKIFEFKETTGTGAFSEVTLAEKATGKLPFAVKCIPKALKGKSSIEINEIAVLR 74
QY 76 MKHGPNILOLVDFVTRKREYFIFELATGREVFDMILDOGYSEBDTSNVVQVLEAVAY 135
DB 75 KIKHENIVALIEDIYESPNHLVLMQVSGELFDRIVEGFTKXASTLIQVLDVAVY 134
QY 136 LHSKIVHNLKLENTVYTRNLKNSKIYSDPHLAKLS--NGLIKPQCTPRYLAEVYG 193
DB 135 LHRMGIVHRDLKPENLILYSODEBSKIMISDFGLSMEKGDVMTACGTPGYVAPEVLA 194
QY 194 RQRYGRPYDCAVGMVITLISGNPPFEVEEDVDENHDKNLFKRLAGDYEPDSPYMD 253
DB 195 QKPYSAVDWCSIGVAYILLCYPPFYDE-----NDSKLPQILKAEVFPDSFYWD 246
QY 254 DISQAKDLVTRIMEVEDQRTIAERAIHSEWISGNAASDKNIKQGVCAQIEKNFARAKW 313
DB 247 DISDSAKDPIRLNMEKDPNKRYTCEQAAHPWLAGDTALNKNIHESVSAQIRKNFAKSKW 306
QY 314 KKAVRTTLMKRLR-----APEGSSTAAGS-----ASADTATPGA-----AGATATAAAS 360
DB 307 RQAFNATAVVRHNRKQLGSSLSNVAVSSTLSLSAQDCIAPSTLCSFISSSGVSGGV 366
QY 361 GATSAPEDGAARAKS 376
DB 367 GAERRPRTTVAVHS 382

RESULT 7
US-09-579-664B-10
Sequence 10, Application US/09579664B
Patent No. 6514719
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Vitca, G. Duke
APPLICANT: Martin, Unja
APPLICANT: Anderson, Dirk M.

TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

FILE REFERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 355
TYPE: PRT
ORGANISM: Mus musculus
US-09-579-664B-10

Query Match 29.6%; Score 764; DB 4; Length 355;
Best Local Similarity 43.0%; Pred. No. 5.3e-48;
Matches 142; Conservative 78; Mismatches 100; Indels 10; Gaps 2;

QY 16 QPSEVTDRYDLGVITKEEFCEIFRAKDKTTGKLTCKKFKQKDRGRKRAKANEIGILK 75
DB 15 QADIDKIFEFKETTGTGAFSEVTLAEKATGKLPFAVKCIPKALKGKSSIEINEIAVLR 74
QY 76 MKHGPNILOLVDFVTRKREYFIFELATGREVFDMILDOGYSEBDTSNVVQVLEAVAY 135
DB 75 KIKHENIVALIEDIYESPNHLVLMQVSGELFDRIVEGFTKXASTLIQVLDVAVY 134
QY 136 LHSKIVHNLKLENTVYTRNLKNSKIYSDPHLAKLS--NGLIKPQCTPRYLAEVYG 193
DB 135 LHRMGIVHRDLKPENLILYSODEBSKIMISDFGLSMEKGDVMTACGTPGYVAPEVLA 194
QY 194 RQRYGRPYDCAVGMVITLISGNPPFEVEEDVDENHDKNLFKRLAGDYEPDSPYMD 253
DB 195 QKPYSAVDWCSIGVAYILLCYPPFYDE-----NDSKLPQILKAEVFPDSFYWD 246
QY 254 DISQAKDLVTRIMEVEDQRTIAERAIHSEWISGNAASDKNIKQGVCAQIEKNFARAKW 313
DB 247 DISDSAKDPIRLNMEKDPNKRYTCEQAAHPWLAGDTALNKNIHESVSAQIRKNFAKSKW 306
QY 314 KKAVRTTLMKRLR-----APEGSSTAAGS-----ASADTATPGA-----AGATATAAAS 360
DB 307 RQAFNATAVVRHNRKQLGSSLSNVAVSSTLSLSAQDCIAPSTLCSFISSSGVSGGV 366

RESULT 8
US-09-733-388-4

Sequence 4, Application US/09733388
Patent No. 6602698
GENERAL INFORMATION:
APPLICANT: Donoho, Greg
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Abulin, Alejandro
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/09/733,388
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
US-09-733-388-4

Query Match 29.2%; Score 754.5; DB 4; Length 356;
Best Local Similarity 40.1%; Pred. No. 2.6e-47;
Matches 147; Conservative 84; Mismatches 109; Indels 27; Gaps 4;

QY 16 QPSEVTDRYDLGVITKEEFCEIFRAKDKTTGKLTCKKFKQKDRGRKRAKANEIGILK 75


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Db      15 QAEIDIKIIFEFKELTGAFSEVVLAEKATGKLFVAKCIPKALKGKSSINENIAVLR 74
QY      76 MVKPNILQADVTVTRKEVYFIPELATGREVPMDLDQGYSEBDTSNVVROYLEAVAY 135
Db      75 KIKHENIVALEDIYESPNHLVYVQVYSGGELFRIYKGFYTKDASTIIRQVLDVAVY 134
QY      136 LHSIKIVHRNKLBNLYVYNLKNKSKIIVISDFHLAKLE--NGLIKEPCGPEYLAPVVG 193
Db      135 LHRMGIVHRDLKPNLKYSGDESKIMISDFGLSKNEGKQDVSTACGPGVYAPVLA 134
QY      194 KQKRGPRVDCALIGVIMTILISGNPFYEEVEEDYENHDKNLFKRLAADYEPDSPYWD 253
Db      195 QKPYSKAVDCMSIGIVAYILLGYPFYDE-----NDSKLFEEQILKAKEYEFDSPYWD 246
QY      254 DISQAADLVTRLMEVODORTAEBAISHENISGNAASDKTKDGYCAQIKENKPARAKY 313
Db      247 DISQAADLVTRLMEVODORTAEBAISHENISGNAASDKTKDGYCAQIKENKPARAKY 305
QY      314 KKAIVTTIMKRLRAPQSSSTAASATDTATPGAAGATAAASGATSAPGDAARA 373
Db      306 KQAPNATAVVRHMKLHGLSSLDSSNAS-----VSSLSLSAQKDCAYV 349
QY      374 AKSDNVA 380
Db      350 AKPESTLS 356

```

RESULT 9
US-09-230-896C-29
Sequence 29, Application US/09230896C
Patent No. 6635479
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Sutcliffe, et al.
TITLE OF INVENTION: Hypochalams-Specific Polypeptides
FILE REFERENCE: TSRI-548.1
CURRENT APPLICATION NUMBER: US/09/230,896C
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: 60/023,220
PRIOR FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 358
TYPE: PRT
ORGANISM: ratus ratus
US-09-230-896C-29

Query Match 27.7%; Score 715; DB 4; Length 358;
Best Local Similarity 42.3%; Pred. No. 2e-44;
Matches 142; Conservative 72; Mismatches 112; Indels 10; Gaps 3;

```

QY      16 QPSEVTRDYDGOYIKTEEFCEIFRAKDKTKGLTKCKKQKRGKRVKRAKNEIGILK 75
Db      7 QTEDISSVYERREKLGSAFSEVWLAQERGSANLVALKCIPIKALRGKALVENEIAVLR 66
QY      76 MVKPNILQADVTVTRKEVYFIPELATGREVPMDLDQGYSEBDTSNVVROYLEAVAY 135
Db      67 RISHPNIVALEDVHESBSHLVLAELVTGGELFRIYKGFYTKDASHLVGVYLAIVSY 126
QY      136 LHSIKIVHRNKLBNLYVYNLKNKSKIIVISDFHLAKLENG-LIKEPGCTPEYLAPVVG 194
Db      127 LHSIGIVHRDLKPNLKYATPFEDSKIMVSDFGLSKIQAQNMGLTAGCTGYVAPBELLEQ 186
QY      195 QKRGPRVDCALIGVIMTILISGNPFYEEVEEDYENHDKNLFKRLAADYEPDSPYWD 254
Db      187 KPYKRAVDVWALGVISYILLGYPFYDE-----SDPELFQILRASVEYFDSPPWMD 238
QY      255 ISOAKLVLTATLMEVEDORTAEBAISHENISGNAASDKTKDGYCAQIKENKPARAKY 314
Db      239 ISESAQDIFRHLTRDPQKRTCCQALQHLWISGDALDRDILGVSVEEQIKNFARTHMK 298

```

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QY      315 KKAIVTTIMKRLRAPQSSSTAASATDTATPGA 349
Db      299 RAFNATSPFRHTRKLGQSPGEGEASRQGMTRSHPG 334

```

RESULT 10

```

US-08-878-989-5
Sequence 5, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT06
CLONE: 827431
US-08-878-989-5

```

Query Match 24.9%; Score 642.5; DB 2; Length 343;
Best Local Similarity 40.6%; Pred. No. 3.6e-39;
Matches 126; Conservative 69; Mismatches 106; Indels 9; Gaps 2;

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QY      19 EYTDVRYDGOYIKTEEFCEIFRAKDKTKGLTKCKKQKRGKRVKRAKNEIGILK 78
Db      10 DISSVYERREKLGSAFSEVWLAQERGSANLVALKCIPIKALRGKALVENEIAVLR 69
QY      79 HNNILQADVTVTRKEVYFIPELATGREVPMDLDQGYSEBDTSNVVROYLEAVAYLHS 138
Db      70 HNNIVALEDVHESBSHLVLAELVTGGELFRIYKGFYTKDASHLVGVYLAIVSYLHS 129
QY      139 LKIVHRNKLBNLYVYNLKNKSKIIVISDFHLAKLENG-LIKEPGCTPEYLAPVVG 197
Db      130 LQIVHRDLKPNLKYATPFEDSKIMVSDFGLSKIQAQNMGLTAGCTGYVAPBELLEQ 189

```


US-09-975-326-2
; Sequence 2, Application US/09975326
; Patent No. 6476210
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mabur, Brian
; TITLE OF INVENTION: No. 6476210e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0254-USA
; CURRENT APPLICATION NUMBER: US/09/975,326
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/239,821
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 766
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-975-326-2

Query Match 22.5%; Score 580.5; DB 4; Length 766;
Best local Similarity 30.3%; Pred. No. 3,3e-34;
Matches 146; Conservative 72; Mismatches 151; Indels 113; Gaps 10;

QY 15 NOPSEVTDYDLDGVITKEEFCEIFRAKDKTGLTKLTKCKFQKRDGRKVRKAANKNEIGIL 74
DB 385 SESSTLEKXKIGKVGDNFAVKECIDRSTGEFALKIIDKACCGKEHLIENEVSIL 444
QY 75 KKKKPNIIQVDFVTRKEYRIFLELATGREVFMILDQGYSERDTSNVRQVLEAVA 134
DB 445 RRYKHPNIIIMLVEEMETATELFLVMEIYVGDLPALISSTYTERDGSAMVYNLANLR 504
QY 135 YLHSLKIVRNKLENTLV--YYNRLKNSKIVISDPHLAKLENGLIKBPCEPYLEAPEV 191
DB 505 YLHGSLIVRDIKPEMLVCEYPDGTSK--LGDGLATVVEGFLPYTCGPTVVAPEI 562
QY 192 VGRQRYGPEVDCWALGVIIYIILSGNPPYEEVEEDDYENHDKNLFRKILAGDYEFDSPY 251
DB 563 IAEITGGLKVDIMAGVITYIILCGFPFRSE-----NNLGEDLPDQILAKLEFPAPY 616
QY 252 WDDISQAAYDLVTRLMVEQDQRTIAEAIISHEWISGNAPASDKNITKGYCAQIEKNFAPA 311
DB 617 WDIITDSAKELISQMLQVWVEARCTAGQILSHPWVSDDASQENMQAEVYTGKIKOHFNNA 676
QY 312 KMKKAVRTTLMKRLAPRQSSPAAGSA---SATDTATPGAAGATAAASGATSAPEG 368
DB 677 -----LPRKNSSTTGVSIVKNTALD-----KEG 699
QY 369 DABAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSVTPDTSATP 428
DB 700 QT-----FCSKHODSGRFGME-----PISPY----- 721
QY 429 ATDGRATPATESVTPTTOSAMLATKAATPEPANAQPDSTAPEGATGAPSSKGEZA 488
DB 722 -----PPSVVE-----IPVGEAVVPAPFPPESTPHCPFAAPGGER 757
QY 489 AG 490
DB 758 AG 759

Search completed: April 23, 2004, 15:50:50
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:43:58 ; Search time 59 Seconds
(without alignments)
2399.259 Million cell updates/sec

Title: US-10-669-689-2
Perfect score: 2581
Sequence: 1 MPFGCVTLGDKKNYNQPSV.....SSKGEAAAGYAQESQREAS 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      1586107 segs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

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Database :
1: Geneseqp29u004:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004as:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2581	100.0	501	5	AA#48279	AA#48279 Human prot
2	2577	99.8	501	4	AA#11783	AA#11783 Human kin
3	2566	99.4	501	4	AA#38988	AA#38988 Human pol
4	2566	99.4	501	4	AA#67539	AA#67539 Amino acid
5	2563	99.3	501	4	AA#93379	AA#93379 Human pol
6	2403	93.1	473	4	AB#52788	AB#52788 Human sig
7	2402.5	93.1	470	4	AA#93404	AA#93404 Human pol
8	2402.5	93.1	470	4	AA#20327	AA#20327 Human prot
9	2398.5	92.9	470	4	AA#93679	AA#93679 Human pol
10	2391.5	92.7	470	4	AA#38987	AA#38987 Human pol
11	1403.5	54.4	284	3	AA#42348	AA#42348 Human ORF
12	1255.5	48.6	289	4	AB#52789	AB#52789 Human sig
13	978	37.9	187	4	AB#52790	AB#52790 Human sig
14	966	37.4	204	4	AA#87207	AA#87207 Novel cent
15	852	33.0	219	4	AA#17267	AA#17267 Novel sig
16	852	33.0	219	4	AA#87517	AA#87517 Novel cent
17	852	33.0	219	7	AB#93975	AB#93975 Human prot
18	793	30.7	370	6	AA#34492	AA#34492 Human cent
19	775	30.0	332	7	AD#C1504	AD#C1504 Calcium/C
20	771	29.9	317	5	AB#68794	AB#68794 Human CAM
21	771	29.9	357	4	AA#11768	AA#11768 Human kin
22	767.5	29.7	385	4	AA#34482	AA#34482 Human pol
23	767.5	29.7	385	4	AA#84359	AA#84359 Amino acid
24	766	29.7	357	4	AA#03508	AA#03508 Human prot
5	764	29.6	355	4	AA#50055	AA#50055 Myrline De

26	764	29.6	355	AAE11777	AAE11777	Human	kin
27	764	29.6	355	AA412668	AA412668	Human	pol
28	764	29.6	355	AB808178	AB808178	Human	Cam
29	754.5	29.12	356	AA843660	AA843660	Human	Cam
30	748.5	29.0	389	AAy68793	AAy68793	Amino	act
31	748.5	29.0	405	AB581876	AB581876	Drosophila	
32	747.5	29.0	476	AAE22764	AAE22764	Human	cal
33	747.5	29.0	476	AB569793	AB569793	Human	Pro
34	747.5	29.0	476	AB563931	AB563931	Human	Pro
35	747.5	29.0	476	AD56387	AD56387	Human	Pro
36	747.5	29.0	476	AD445328	AD445328	Human	pol
37	747.5	29.0	497	AA415447	AA415447	Human	pol
38	746	28.9	460	AB669792	AB669792	Human	Cal
39	738	28.6	567	AA319761	AA319761	Human	pol
40	727.5	28.12	503	AB605760	AB605760	Novel	hum
41	720	27.9	309	AD56388	AD56388	Rat	Prote
42	720	27.9	309	AD445326	AD445326	Rat	Prote
43	720	27.9	309	AD56385	AD56385	Rat	Prote
44	720	27.9	309	AD446031	AD446031	Rat	Prote
45	718	27.8	326	AAE32426	AAE32426	Human	kin

ALIGNMENTS

RESULT 1

ID AAM48279 standard; protein; 501 AA.

AC AAM48279;

DT 03-APR-2002 (first entry)

Human protein kinase

KW Human; protein kinase; enzyme; brain; Lung; hippocampus;

KW calmodulin-binding kinase; gene therapy.

OS Homo sapiens

PN WO200192492-

PD 06-DEC-2001.

PF 30-MAY-2001; 2001WC-US017327.

PR 30-MAY-2000; 2000US-0207281P.

2000

110

0677770 / 13

XX
X

DR N-PSDB; ABA95682.

PT New calmodulin-blind:

screening for compounds

PS Claim 1; Fig 2; 15pp; English

The present sequence is the pr

the adult brain), lung and in

coating sequence can be used as the starting point for the design of the coating sequence in the

modulate kinase activity in cere-

disorder associated with nucle

cc particularly biological and political

CC the kinase in cells and tissues that express it, as antisense constructs
CC to control kinase gene expression in cells, tissues or organisms, and in
CC gene therapy

XX Sequence 501 AA:

Query Match 100.0%; Score 2581; DB 5; Length 501;
Best Local Similarity 100.0%; Pred. No. 4,8e-187;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFGCVTLGDKKNYNQPSSEVTDRIYDLGVYIKTEBCEIFRAKDKTTGKLTCKKFKQKRDG 60
DB 1 MPFGCVTLGDKKNYNQPSSEVTDRIYDLGVYIKTEBCEIFRAKDKTTGKLTCKKFKQKRDG 60
QY 61 RRVRAAKKEIGILKVVKNHNTLQVDVFTVRKEVIFLELATGSEVDMILDDGYSER 120
DB 61 RRVRAAKKEIGILKVVKNHNTLQVDVFTVRKEVIFLELATGSEVDMILDDGYSER 120
QY 121 DTSNVVQVLEAVVYLSKIVHRNLKLENYNRLKNSKIVISDFHLATLENGILKEP 180
DB 121 DTSNVVQVLEAVVYLSKIVHRNLKLENYNRLKNSKIVISDFHLATLENGILKEP 180
QY 161 CGTPEYLAPEVVGQRQYGRPVDCMAIGVIMYLLSGNPPFEVEEDDYENHDKNLPKRI 240
DB 161 CGTPEYLAPEVVGQRQYGRPVDCMAIGVIMYLLSGNPPFEVEEDDYENHDKNLPKRI 240
QY 241 IAGDVEFQSPYWDISQAKDLYTFLMEVEDQRTAEBAISHETISGNAASDKIKXGV 300
DB 241 IAGDVEFQSPYWDISQAKDLYTFLMEVEDQRTAEBAISHETISGNAASDKIKXGV 300
QY 301 CAQIKENFPAKAKKAVRTTLMKRLBAPESGSTAAASATDPTGGAAGATAAAS 360
DB 301 CAQIKENFPAKAKKAVRTTLMKRLBAPESGSTAAASATDPTGGAAGATAAAS 360
QY 361 GATSAPEGDAABAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
DB 361 GATSAPEGDAABAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
QY 421 VTDRSATPATDGRATPATIEESTVPTTQSSAMLTATAATPEPAMAQDPTNAPEGATQAP 480
DB 421 VTDRSATPATDGRATPATIEESTVPTTQSSAMLTATAATPEPAMAQDPTNAPEGATQAP 480
QY 481 PSSKGBEAGVAGQESQREAS 501
DB 481 PSSKGBEAGVAGQESQREAS 501

RESULT 2

AAE11783
ID AAE11783 standard, protein, 501 AA.

XX AAE11783;

DT 18-DEC-2001 (first entry)

XX Human kinase (PKIN)-17 protein.

XX Human kinase (PKIN)-17 protein.
XX Human kinase (PKIN); gene therapy; adenocarcinoma; immune deficiency; gout;
XX cancer; allergy; sarcoma; leukemia; acquired immune deficiency syndrome;
XX AIDS; Addison's disease; microbial infection; inflammation; osteoporosis;
XX myasthenia gravis; cardiovascular disease; myocardial infarction; anaemia;
XX seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder;
XX lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease;
XX obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular;
XX antimicrobial; cytoskeletal; antiinflammatory; asthma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 25..276
FT /note= "Protein kinase domain"
FT 35..277

FT /note= "Protein kinase domain"
FT Domain 37..286
FT /note= "Eukaryotic protein kinase domain"
FT Domain 135..153
FT /note= "Tyrosine kinase catalytic domain"
FT Domain 201..223
FT /note= "Tyrosine kinase catalytic domain"

XX MO2001B1555-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012992.

XX 20-APR-2000; 2000US-0199021P.

XX 28-APR-2000; 2000US-0200226P.

XX 03-MAY-2000; 2000US-0202339P.

XX 11-MAY-2000; 2000US-0203505P.

XX 18-MAY-2000; 2000US-0205564P.

XX 26-MAY-2000; 2000US-0207739P.

XX 01-JUN-2000; 2000US-0208795P.

XX (INCY-) INCYTE GENOMICS INC.

XX Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB;
XX Bandman O, Lu DM, Lal P, Burford N, Khan FA, Wala NK, Yao MG;
XX Patterson C, Burrill JD, Marcus GA, Zingler KA, Reardon SA, Lu Y;
XX Pi Policy J, Thornton W, Tang YT, Hafalila A, Elliott VS, Baughn MR;
XX Pi Walsh RT, Ramkumar J, Borowsky ML, Au-Young J, Hillman J;
XX Gururajan R;

XX WPI; 2001-611740/70.

XX DR N-PSDB; AAD18832.

XX Human kinases and nucleic acids, useful for preventing diagnosing and
XX treating cancers, inflammation and immune disorders.

XX PS Claim 1, Page 148-149; 166pp; English.

XX The present invention relates to human kinases (PKIN) and the nucleic
XX acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is
XX used in the prevention, diagnosis and treatment of diseases cancers,
XX adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease,
XX acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies,
XX gout, microbial infections, cardiovascular disease and/or inflammation,
XX myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial
XX infarction, cataract, growth and development disorder, seizure disorder,
XX pulmonary embolism, Gaucher's disease, lipid disorder, lipid storage
XX disease, Pick's disease, Tay-Sachs disease, renal disease and obesity.
XX PKIN may be used to treat disorders associated with decreased PKIN
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of PKIN by expressing inactive proteins or to
XX supplement the patient's own production of PKIN. PKIN nucleic acids may be
XX used to produce the PKIN polypeptide, by inserting the nucleic acids into
XX a host cell and culturing the cell to express the protein. PKIN nucleic
XX acid and its complementary sequences may also be used as DNA probes in
XX diagnostic assays to detect and quantitate the presence of similar
XX nucleic acid sequences in samples and therefore which patients may be in
XX need of restorative therapy. The present sequence is human PKIN-17
XX protein

XX Sequence 501 AA;

Query Match 99.8%; Score 2577; DB 4; Length 501;
Best Local Similarity 99.8%; Pred. No. 9,6e-187;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPFGCVTLGDKKNYNQPSSEVTDRIYDLGVYIKTEBCEIFRAKDKTTGKLTCKKFKQKRDG 60
DB 1 MPFGCVTLGDKKNYNQPSSEVTDRIYDLGVYIKTEBCEIFRAKDKTTGKLTCKKFKQKRDG 60
QY 61 RRVRAAKKEIGILKVVKNHNTLQVDVFTVRKEVIFLELATGSEVDMILDDGYSER 120

Db 61 RYRKAQKAEIGILKRVKHPNIIQLVDVFTVTRKEYIFIELATGREVFWIIDQGYSER 120
 QY 121 DTSNVROYLEAVAYLHSLKIVHRNKLLENVYNNRLKNSKIYISDFHLAKLENGLKEP 180
 Db 121 DTSNVROYLEAVAYLHSLKIVHRNKLLENVYNNRLKNSKIYISDFHLAKLENGLKEP 180
 QY 181 CGTPEYLAEVVGROQYGRPDCAIIVIMYLLSGNPPFYEEBEDDYENHDKLFRKI 240
 Db 181 CGTPEYLAEVVGROQYGRPDCAIIVIMYLLSGNPPFYEEBEDDYENHDKLFRKI 240
 QY 241 LAGDYEPFSDPYWDISQAADLVTRLMVEVQDORITAEBAISHEMIISGNAASDKNIKGV 300
 Db 241 LAGDYEPFSDPYWDISQAADLVTRLMVEVQDORITAEBAISHEMIISGNAASDKNIKGV 300
 QY 301 CAQIEKNFAPAKKKAQVAVTTLMKRLRAPBQSTAAQASATDITPAGAGATPAAAS 360
 Db 301 CAQIEKNFAPAKKKAQVAVTTLMKRLRAPBQSTAAQASATDITPAGAGATPAAAS 360
 QY 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 Db 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 QY 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAPGATGAP 480
 Db 421 ATDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAPGATGAP 480
 QY 481 PSSKGEBAAGYAQESQREBAS 501
 Db 481 PSSKGEBAAGYAQESQREBAS 501

RESULT 3

AA038988 standard; protein; 501 AA.

AA038988;

22-OCT-2001 (first entry)

Human polypeptide SEQ ID NO 2133.

Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

Homo sapiens.

MO20015312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US034263.

23-DEC-1999; 99US-00471275.
 21-JAN-2000; 2000US-00488725.
 25-APR-2000; 2000US-00552317.
 20-JUN-2000; 2000US-00598042.
 19-JUL-2000; 2000US-00620312.
 03-AUG-2000; 2000US-00653450.
 14-SEP-2000; 2000US-00662191.
 19-OCT-2000; 2000US-00693036.
 29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

Tang Y.T., Liu C., Aouni V., Chen R., Ma Y., Qian X.B., Ren F., Wang D., Wang Z., Wehrman T., Xu C., Xue A.J., Yang Y., Zhang J., Zhao Q., Zhou F., Goodrich R., Drmanac R.T.;
 WPI; 2001-442253/47.

DR N-PSDB; AA158144.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 4; SEQ ID NO 2133; 10078pp; English.
 CC The invention relates to human nucleic acids (AA15798-AA161369) and the
 CC encoded polypeptides (AA038642-AA042213) with noctropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 501 AA;

Query Match 99.4%; Score 2566; DB 4; Length 501;
 Best Local Similarity 99.4%; Pred. No. 6.5e-166;
 Matches 498; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPFGCVTLGDKKNYNQPSVETDRYDLQGVITKEBFCEIFRAKDTYTGKATCKKFKQRDG 60
 Db 1 MPFGCVTLGDKKNYNQPSVETDRYDLQGVITKEBFCEIFRAKDTYTGKATCKKFKQRDG 60
 QY 61 RYRKAQKAEIGILKRVKHPNIIQLVDVFTVTRKEYIFIELATGREVFWIIDQGYSER 120
 Db 61 RYRKAQKAEIGILKRVKHPNIIQLVDVFTVTRKEYIFIELATGREVFWIIDQGYSER 120
 QY 121 DTSNVROYLEAVAYLHSLKIVHRNKLLENVYNNRLKNSKIYISDFHLAKLENGLKEP 180
 Db 121 DTSNVROYLEAVAYLHSLKIVHRNKLLENVYNNRLKNSKIYISDFHLAKLENGLKEP 180
 QY 181 CGTPEYLAEVVGROQYGRPDCAIIVIMYLLSGNPPFYEEBEDDYENHDKLFRKI 240
 Db 181 CGTPEYLAEVVGROQYGRPDCAIIVIMYLLSGNPPFYEEBEDDYENHDKLFRKI 240
 QY 241 LAGDYEPFSDPYWDISQAADLVTRLMVEVQDORITAEBAISHEMIISGNAASDKNIKGV 300
 Db 241 LAGDYEPFSDPYWDISQAADLVTRLMVEVQDORITAEBAISHEMIISGNAASDKNIKGV 300
 QY 301 CAQIEKNFAPAKKKAQVAVTTLMKRLRAPBQSTAAQASATDITPAGAGATPAAAS 360
 Db 301 CAQIEKNFAPAKKKAQVAVTTLMKRLRAPBQSTAAQASATDITPAGAGATPAAAS 360
 QY 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 Db 361 GATSAPEGDAARAASDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 QY 421 VTDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAPGATGAP 480
 Db 421 ATDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDSTAPGATGAP 480
 QY 481 PSSKGEBAAGYAQESQREBAS 501
 Db 481 PSSKGEBAAGYAQESQREBAS 501

RESULT 4

AA067539 standard; protein; 501 AA.

AA067539;

26-NOV-2001 (first entry)

XX	DE	Amino acid sequence of human kinase 2504.	
XX	KW	Human, kinase; 2504; 15977; 14760; cellular proliferative disorder;	
XX	KW	cellular differentiative disorder; neural disorder; immune disorder;	
XX	KW	cardiovascular disorder; liver disorder; skin disorder;	
XX	KW	skeletal muscle disorder; bone metabolism; cardiovascular disorder;	
XX	KW	viral disease; pain; metabolic disorder; blood vessel disorder;	
XX	KW	hepatic disorder; liver disorder.	
OS	XX	Homo sapiens.	
XX	XX		
XX	XX	Key	Location/Qualifiers
FT	FT	Modified-site	7..10
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	21..23
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Domain	24..286
FT	FT	Domain	/note= "serine/threonine kinase domain"
FT	FT	Domain	37..286
FT	FT	Domain	/note= "eukaryotic protein kinase domain"
FT	FT	Modified-site	46..48
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	51..53
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	59..62
FT	FT	Modified-site	/note= "predicted amidation site"
FT	FT	Modified-site	91..94
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	91..93
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	103..106
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	103..105
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	118..121
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	118..120
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	127..135
FT	FT	Modified-site	/note= "predicted tyrosine kinase phosphorylation site"
FT	FT	Modified-site	138..140
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	276..279
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	288..293
FT	FT	Modified-site	/note= "predicted N-myristoylation site"
FT	FT	Modified-site	292..294
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	341..344
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	349..354
FT	FT	Modified-site	/note= "predicted N-myristoylation site"
FT	FT	Modified-site	364..367
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	422..424
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	470..473
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	482..484
FT	FT	Modified-site	/note= "predicted protein kinase C phosphorylation site"
FT	FT	Modified-site	483..486
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
FT	FT	Modified-site	484..491
FT	FT	Modified-site	/note= "predicted tyrosine kinase phosphorylation site"
FT	FT	Modified-site	495..498
FT	FT	Modified-site	/note= "predicted casein kinase II phosphorylation site"
XX	XX		
XX	XX	WO200164905-A2.	
XX	XX	07-SEP-2001.	
XX	XX	28-FEB-2001; 2001WO-US006525.	

XX		PR	29-FEB-2000; 2000US-0186061P.	
XX		PA	(MILL-) MILLENNIUM PHARM INC.	
XX	F1	P1	Olandt PJ, Kapeller-Libermann R, Meyers RA;	
XX	DR	WI	MPJ; 2001-570697/64.	
XX	DR	N-PSDB	AHH78261.	
XX	PT		New protein kinase family polypeptides for treating hemtopietic neoplastic disorders, immune disorders, cardiovascular disorders and disorders of blood vessels.	
XX	PS		Claim 9; Fig 1A-B; 145pp; English.	
XX	CC		The present sequence represents human kinase 2504. The specification also describes kinases 15977 and 14760. The kinase polypeptides and polymolecites are used to treat cellular proliferative or differentiative disorders, neural disorders, immune disorders, cardiovascular disorders, liver disorders, skin disorders and skeletal muscle disorders. They may also be used for controlling disorders associated with bone metabolism, cardiovascular disorders, viral diseases, pain or metabolic disorders, blood vessel disorders, and hepatic or liver disorders	
SQ			Sequence 501 AA:	
QY	Query Match	99.4%; Score 2566; DB 4; Length 501;		
Bst Local Similarity	99.6%; Pred. No. 6.5e-186;			
Matches 499; Conservative	0; Mismatches 2; Indels 0; Gaps 0			
DG	1 MPFGCVTLGDKNKNOPESEVTDYDLGVITEEFCEFRAKDKTTGKLHCKCFQRKD	60		
DG	1 MPFGCVTLGDKNKNOPESEVTDYDLGVITEEFCEFRAKDKTTGKLHCKCFQRKD	60		
DG	61 RKVKRAANEIGILKMVHPNLTLDVFVTRKEYFIFLELATGRVEDWILDQGYSER	120		
DG	61 RKVKRAANEIGILKMVHPNLTLDVFVTRKEYFIFLELATGRVEDWILDQGYSER	120		
DG	121 DTSNVROVLEAVAYLHSKLVHNLKLENVYNNRLNKSTIVSDPHLAKLENGLKEP	180		
DG	121 DTSNVROVLEAVAYLHSKLVHNLKLENVYNNRLNKSTIVSDPHLAKLENGLKEP	180		
DG	161 CGTEBYLAPEVVGQRYSRPPDCNAIGTVYLLSGNPFEYVEEDYENHKULFKFI	240		
DG	161 CGTEBYLAPEVVGQRYSRPPDCNAIGTVYLLSGNPFEYVEEDYENHKULFKFI	240		
DG	241 LAGDYEPDPSYWDNISQAADLVTRLMEVEEODRTTAEALSHEWISGNAA SDKNIKDG	300		
DG	241 LAGDYEPDPSYWDNISQAADLVTRLMEVEEODRTTAEALSHEWISGNAA SDKNIKDG	300		
DG	301 CAQEIKNFARAKWKXAVVTLMKRLRAPBOSSTMAASANTDTATGAAGAATAAAS	360		
DG	301 CAQEIKNFARAKWKXAVVTLMKRLRAPBOSSTMAASANTDTATGAAGAATAAAS	360		
DG	361 GATSAPEBDARAASNDVAPADRATPATGSATPATDSITPATDSITPATGSVTP	420		
DG	361 GATSAPEBDARAASNDVAPADRATPATGSATPATDSITPATDSITPATGSVTP	420		
DG	421 VTDESATPATGSRATPATESVTPPTQSAMLATYAATPEBAMAQPDSTAPEGATGAP	480		
DG	421 ATDEATPATGSRATPATESVTPPTQSAMLATYAATPEBAMAQPDSTAPEGATGAP	480		
DG	481 PSSKGEEAAGYAQESOREAS 501			
DG	481 PSSKGEEAAGYAQESOREAS 501			
RESULT 5				
ID	AAAG3379			
XX	standard; protein; 501 AA.			

AC AAW93379;
 XX 06-NOV-2001 (first entry)
 XX Human polypeptide, SEQ ID NO: 2957.
 XX Human, full length cDNA, cDNA synthesis; oligo-capping.
 XX Homo sapiens.
 XX EPI130094-A2.
 XX 05-SEP-2001.
 XX 07-JUL-2000; 2000EP-00114089.
 XX 08-JUL-1999; 99JP-00194486.
 XX 11-JAN-2000; 2000JP-00118774.
 XX 02-MAY-2000; 2000JP-00183765.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI; 2001-524255/58.
 XX N-PSDB; AAK94299.
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 XX Claim 8; SEQ ID NO 2957; 1380bp + Sequence Listing; English.
 XX The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 501 AA;
 Query Match 99.3%; Score 2563; DB 4; Length 501;
 Best Local Similarity 99.6%; Pred. No. 1.1e-165;
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGGVITKEEFCIEFRAXDKTTGKLTCKKFKQRDG 60
 DB 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGGVITKEEFCIEFRAXDKTTGKLTCKKFKQRDG 60
 QY 61 RKVRKAANEIGILKMTVGHENILQLVDFVTRKEVFIFLELATGREVPDWILDDGYYSER 120
 DB 61 RKVRKAANEIGILKMTVGHENILQLVDFVTRKEVFIFLELATGREVPDWILDDGYYSER 120
 QY 121 DTSNVVRQVLAVALYHSLKIVHNLKLENVYNNRLKNSIVISDPHLAELNGLLKEP 180
 DB 121 DTSNVVRQVLAVALYHSLKIVHNLKLENVYNNRLKNSIVISDPHLAELNGLLKEP 180
 QY 181 CGTPEYLAPEVVGRORYRPPVDCMAIGVIMTILSGNPPFEVEEEDDYENHNDLPRXI 240
 DB 181 CGTPEYLAPEVVGRORYRPPVDCMAIGVIMTILSGNPPFEVEEEDDYENHNDLPRXI 240
 QY 241 LAGDVEFDSPYWDISQAADLVRLMEVEODORTAEASISHEMISGNAASDNKIDGV 300
 DB 241 LAGDVEFDSPYWDISQAADLVRLMEVEODORTAEASISHEMISGNAASDNKIDGV 300
 QY 301 CAQIEKNPAPAKMKKAVRTTLMKRLRAPDSSTAAASATDTATPAAAGATAAAS 360

DB 301 CAQIEKNPAPAKMKKAVRTTLMKRLRAPDSSTAAASATDTATPAAAGATAAAS 360
 QY 361 GATSAPEDGAPAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 DB 361 GATSAPEDGAPAAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP 420
 QY 421 VTDRSATPATDGRATPATTEESTVPTTOSAMTATCAATPEPMAQPDSTAPEGATGAP 480
 DB 421 ATDRSATPATDGRATPATTEESTVPTTOSAMTATCAATPEPMAQPDSTAPEGATGAP 480
 QY 481 PSSKGEAAGYAQESQREAS 501
 DB 481 PSSKGEAAGYAQESQREAS 501
 RESULT 6
 ABUS2788
 ID ABUS2788 standard; protein; 473 AA.
 XX
 AC ABUS2788;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Human signal transduction-associated protein from DKFZphb2_82e4.
 XX
 KM Human; gene therapy; vaccine; disease treatment; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO200112659-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 18-AUG-2000; 2000MO-IB001496.
 XX
 PR 18-AUG-1999; 99US-0149499P.
 PR 28-SEP-1999; 99US-0156503P.
 XX
 PA (GEMU-) GERMAN HUMAN GENOME PROJECT.
 XX
 PI Wiemann S;
 XX
 DR WPI; 2001-327840/34.
 DR N-PSDB; ABX71280.
 XX
 PT Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies.
 XX
 PS Claim 21; Page 353; 1095pp; English.
 XX
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a
 CC polypeptide described in the disclosure of the invention
 XX
 SQ Sequence 473 AA;
 Query Match 93.1%; Score 2403; DB 4; Length 473;
 Best Local Similarity 94.2%; Pred. No. 1.4e-173;
 Matches 472; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
 QY 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGGVITKEEFCIEFRAXDKTTGKLTCKKFKQRDG 60
 DB 1 MPFGCVTLGDKKNYNQPSSEVTDRLDGGVITKEEFCIEFRAXDKTTGKLTCKKFKQRDG 60
 QY 61 RKVRKAANEIGILKMTVGHENILQLVDFVTRKEVFIFLELATGREVPDWILDDGYYSER 120

Db	61	RKRRKAARKAEIGLKKVGHFNLLQVLVDVFRKKEFFLELATGRVFDWILDQGYSSR	120
Qy	121	DTSNVTVRQYLEAVAYLHSLKIYVERNIKLENTLVYNRLNKSKIYISDFHLAKLENGLIKPEP	180
Db	121	DTSNVTVRQYLEAVAYLHSLKIYVERNIKLENTLVYNRLNKSKIYISDFHLAKLENGLIKPEP	180
Qy	181	CGRPETLAPREVVRQCYGRPVDCWALGVIMTLLSGNPFPEVEEEDDYENHDKNLFRKI	240
Db	181	CGRPETL-----GNPFPEVEEEDDYENHDKNLFRKI	212
Qy	241	LAADYEFDSYPYMDISQAADLVTRLMEYEDPQRTTAEASISHEMISGNAASDKNIKQGV	300
Db	213	LAADYEFDSYPYMDISQAADLVTRLMEYEDPQRTTAEASISHEMISGNAASDKNIKQGV	272
Qy	301	CAQIEKNFAPAKKKKAVRVTITMKRLRAPESGSTAAQASASATDTATPGAAGATAAAS	360
Db	273	CAQIEKNFAPAKKKKAVRVTITMKRLRAPESGSTAAQASASATDTATPGAAGATAAAS	332
Qy	361	GAISAPBEGDAARAAKSDNVAPADRSATPATDGSATPATDGSVTATGSIPTATDGSVTP	420
Db	333	GAISAPBEGDAARAAKSDNVAPADRSATPATDGSATPATDGSVTATGSIPTATDGSVTP	392
Qy	421	VTQRSATPATDGSATPATESITVPTQSSAMLATGAATPEPMAAOPDSTAPBEGATQAP	480
Db	393	ATDRSATPATDGSATPATBESITVPTQSSAMLATGAATPEPMAAOPDSTAPBEGATQAP	452
Qy	481	PSSKGEFAAGYAOESQREAS 501	
Db	453	PSSKGEFAAGYAOESQREAS 473	
RESULT 7			
AA93404			
ID	AA93404	standard; protein; 470 AA.	
AC	AA93404;		
DT	06-NOV-2001	(first entry)	
DE	Human polypeptide, SEQ ID NO: 3008.		
OS	Homo sapiens.		
PN	EP130094-A2.		
PD	05-SEP-2001.		
XX	07-JUL-2000; 2000EP-00114089.		
XX	08-JUL-1999; 99JP-00194486.		
XX	11-JAN-2000; 2000JP-0018774.		
XX	02-MAY-2000; 2000JP-00183765.		
XX	(HELI-) HELIX RES INST.		
XX	Ota T, Nishikawa T, Isogai T, Hayashi K, Iehi S, Kawai Y;		
XX	Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;		
XX	WPI; 2001-524255/58.		
XX	N-PSDB; AA94325.		
XX	830 Primers useful for synthesizing full length cDNA clones and their use		
XX	in genetic manipulation.		
XX	Claim 8; SEQ ID NO 3008; 1380bp + Sequence Listing; English.		
XX	The invention relates to primers for synthesizing full length cDNA		
XX	clones. 830 cDNA molecules encoding a human protein have been isolated		
XX	and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have		
XX	been determined. Primers for synthesizing the full length cDNA are useful		

CC for cloning the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
XQ Sequence 470 AA,
XX

Query Match	93.1%;	Score 2402.5;	DB 4;	Length 470;
Best Local Similarity	93.6%;	Pred. No. 1.5e-173;		
Matches 469; Conservative	0;	Mismatches 1;	Indels 31;	Gaps 1

Qy	1	MPGCVTLGADKKNNQNPBSVDRYDLQGVITFEEFCFLFRKQKTTKJTKCKKFORDG	60
Dp	1	MPGCVTLGADKKNNQNPBSVDRYDLQGVITFEEFCFLFRKQKTTKJTKCKKFORDG	60
Qy	61	RKVRKAKKEIGILKNVKNPNILQVDFVFRKEVFFLELATGREVFDWILDQYYSER	120
Dp	61	RKVRKAKKEIGILKNVKNPNILQVDFVFRKEVFFLELATGREVFDWILDQYYSER	120
Qy	121	DTSNVVRQYLEAVAYLHSLKI VHRNKL ENL VYVNRKNSKTVISDFHLAKLENGLIKEP	180
Dp	121	DTSNVVRQYLEAVAYLHSLKI VHRNKL ENL VYVNRKNSKTVISDFHLAKLENGLIKEP	180
Qy	181	CGTPPEYLAPEVVGROGRYPVDCMAIGVIMYILISGNPPEFEEVEEDDYNNHKNLFRKI	240
Dp	181	CGTPPEYLAPEVVGROGRYPVDCMAIGVIMYILISGNPPEFEEVEEDDYNNHKNLFRKI	240
Qy	241	LADYDFEDSPYMDDISQAAKDLYRKLMEVEDDQITLBEALSHEMISGNASPDKNLIDGV	300
Dp	241	LADYDFEDSPYMDDISQAAKDLYRKLMEVEDDQITLBEALSHEMISGNASPDKNLIDGV	300
Qy	301	CAQIEGNFARAKMKKAVRYTTLMKCLRAPESOSTPAAQOSASATDTAPGAAGATAAAS	360
Dp	301	CAQIEGNFARAKMKKAVRYTTLMKCLRAPESOSTPAAQOSASATDTAPGAAGATAAAS	360
Qy	361	GATSAPEGDABARAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP	420
Dp	361	GATSAPEGDABARAKSDNVAPADRSATPATDGSATPATDGSITPATDGSVTP	420
Qy	421	VTRRSATPATDGRATPATBEESTVPTTQSSAMLATKAAATPEPMAAQDSTAPBEATQAP	480
Dp	421	VTRRSATPATDGRATPATBEESTVPTTQSSAMLATKAAATPEPMAAQDSTAPBEATQAP	480
Qy	481	PSKGEBAAGVAAQESOREEAS 501	
Dp	481	PSKGEBAAGVAAQESOREEAS 501	
Qy	450	PSKGEBAAGVAAQESOREEAS 470	
Dp	450	PSKGEBAAGVAAQESOREEAS 470	

RESULT	8	
AA020327		
ID	AA020327	standard; protein; 470 AA.
XX		
AC	AA020327;	
XX		
DT	29-MAY-2001	(first entry)
XX		
DE	Human protein phosphatase and kinase protein-6.	
XX		
KW	Protein phosphatase and kinase protein; PPHK-6; human;	
KW	gastrointestinal disorder; immune system disorder; neurological disorder;	
KW	cell proliferative disorder; cancer; diagnosis; therapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	7
FT		/note="O-phosphorylated"
FT	Modified-site	21
FT		/note="O-phosphorylated"

FT	Region	24..286
FT	/note= "protein kinase signature"	
FT	Domain	25..276
FT	/note= "protein kinase domain signature"	
FT	Modified-site	46
FT	/note= "O-phosphorylated"	
FT	Modified-site	51
FT	/note= "O-phosphorylated"	
FT	Modified-site	91
FT	/note= "O-phosphorylated"	
FT	Modified-site	103
FT	/note= "O-phosphorylated"	
FT	Modified-site	103
FT	/note= "O-phosphorylated"	
FT	Modified-site	118
FT	/note= "O-phosphorylated"	
FT	Domain	135..153
FT	/note= "tyrosine kinase catalytic domain signature"	
FT	Modified-site	135
FT	/note= "O-phosphorylated"	
FT	Modified-site	138
FT	/note= "O-phosphorylated"	
FT	Domain	201..223
FT	Modified-site	276
FT	/note= "tyrosine kinase catalytic domain signature"	
FT	Modified-site	292
FT	/note= "O-phosphorylated"	
FT	Modified-site	341
FT	/note= "O-phosphorylated"	
FT	Modified-site	391
FT	/note= "O-phosphorylated"	
FT	Modified-site	439
FT	/note= "O-phosphorylated"	
FT	Modified-site	451
FT	/note= "O-phosphorylated"	
FT	Modified-site	452
FT	/note= "O-phosphorylated"	
FT	Modified-site	460
FT	/note= "O-phosphorylated"	
FT	Modified-site	464
FT	/note= "O-phosphorylated"	
PN	MO200120004-A2.	
PD	22-MAR-2001.	
XX		
XX	14-SEP-2000; 2000WO-US025515.	
XX		
XX	15-SEP-1999; 99US-0154141P.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
XX		
XX	Yue H, Tang YT, Bandman O, Hillman JT, Baughn MR, Azimzai Y,	
PI	Lu DM;	
DR	WPI: 2001-244811/25.	
DR	N-PSDB; AAF20381.	
XX		
XX		
PT	Novel human protein phosphatase and kinase proteins for diagnosis,	
PT	treatment and prevention of gastrointestinal, immune system, neurological	
PT	and cell proliferative disorders.	
XX		
PS	Claim 5; Page 89-90; 103pp; English.	
CC		
CC	The present sequence is that of novel human protein phosphatase and	
CC	kinase protein PPHKP-6, as predicted from Incyte Clone ID No. 1385073CB1	
CC	(see AAF00481). Tissues that express PPHKP-6 (as a fraction of total	
CC	tissues expressing PPHKP-6) include nervous (0.885) and developmental	
CC	(0.077). Diseases or conditions associated with tissues expressing PPHKP-	
CC	6 (as a fraction of total tissues expressing PPHKP-6) include	
CC	inflammation or trauma (0.384), neurological (0.231) and cancer (0.192).	
CC	The encoded protein shows homology to rat calmodulin-binding protein. The	

CC	invention provides human PPHK-1 to -11 polypeptides (see AAB20322-32)
CC	and polynucleotides (see AAF30476-86). It also provides expression
CC	vectors, host cells, antibodies, agonists and antagonists, as well as
CC	methods for diagnosing, treating or preventing disorders associated with
CC	expression of PPHK, including gastrointestinal disorders, immune system
CC	disorders, neurological disorders and cell proliferative disorders,
CC	including cancer
XX	
SQ	Sequence 470 AA;
Query Match	93.1%; Score 2402.5; DB 4; Length 470;
Best Local Similarity	93.6%; Pred. No. 1.5e-173; Indels 31; Gaps 1;
Matches 469; Conservative	0; Mismatches 1;
Db	
QY	1 MPFGCVLLGDKKNVNOSEVTRDYDLGVITKEEFCEIFRAKDXTTGGKATCKEFOKSDG 60
Db	1 MPFGCVLLGDKKNVNOSEVTRDYDLGVITKEEFCEIFRAKDXTTGGKATCKEFOKSDG 60
QY	61 RKVKAAKNEIGILNQVHPNILLVDVFVTRKEYFLELATGREVDWILDGYSER 120
Db	61 RKVKAAKNEIGILNQVHPNILLVDVFVTRKEYFLELATGREVDWILDGYSER 120
QY	121 DTSNVAVQVEAVALYLSIKIVHNNLKLENVYYNRNLKNSKIYISDFHLAKLENGLIKEP 180
Db	121 DTSNVAVQVEAVALYLSIKIVHNNLKLENVYYNRNLKNSKIYISDFHLAKLENGLIKEP 180
QY	181 CGTEPEYLAPEVWGQRGRPVDCALGIWYIILSGNPFEEYEEDDYENHDKXLFPKI 240
Db	181 CGTEPEYLAPEVWGQRGRPVDCALGIWYIILSGNPFEEYEEDDYENHDKXLFPKI 240
QY	241 LAGDYEDSPYMDDISQAADLVTRLMEVEODORITAEALISHWISGNNAASDXNIKDG 300
Db	241 LAGDYEDSPYMDDISQAADLVTRLMEVEODORITAEALISHWISGNNAASDXNIKDV 300
QY	301 CAQIEKNFAPAKKMKAVRTTLMKRLAPEQSSTPAASASATDTATGAAGAATAAAS 360
Db	301 CAQIEKNFAPAKKMKAVRTTLMKRLAPEQSSTPAASASATDTATGA----- 350
QY	361 GATSAPEGDABAARKSDNVAPADRSATPATDGSATPATDGSVTPTATDGSITPATDGSVTP 420
Db	351 -----ADRSATPATDGSATPATDGSVTPTATDGSITPATDGSVTP 389
QY	421 VTDRSATPATDGRATPATTEESTVEPTTQSSAMLTAKAAATPPAMAOPDSTAPEGATGA 480
Db	390 ATDRSATPATDGRATPATTEESTVEPTTQSSAMLTAKAAATPPAMAQPSTAPEGATGA 449
QY	481 PSSKGEEPAAGYAQESOREEAS 501
Db	450 PSSKGEEPAAGYAQESOREEAS 470
RESULT 9	
AAM93679	
ID	AAM93679 standard; protein; 470 AA.
AC	
AA	AAM93679;
XX	
XX	06-NOV-2001 (first entry)
DT	
XX	Human polypeptide, SEQ ID NO: 3572.
DE	
XX	Human; full length cDNA; cDNA synthesis; oligo-capping.
KM	
XX	Homo sapiens.
OS	
XX	EPI130094-A2.
PN	
XX	05-SEP-2001.
PD	
XX	
PF	07-JUL-2000; 2000EP-00114089.
XX	
PR	08-JUN-1999; 99JP-00194486.
PR	11-JAN-2000; 2000JP-00118774.

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PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isegai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
DR N-PSDB; AAK94614.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
PS Claim 8; SEQ ID NO 3572; 1380bp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesized by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
XX Sequence 470 AA;
SQ
Query Match 92.7%; Score 2398.5; DB 4; Length 470;
Best Local Similarity 93.4%; Pred. No. 3e-173;
Matches 468; Conservative 1; Mismatches 1; Indels 31; Gaps 1;
QY 1 MPFGCVTLGDKKXNNPSEVTDRLDGOVITKEEFCEIFRAKDKTTGKLTCKKFKQRDG 60
DB 1 MPFGCVTLGDKKXNNPSEVTDRLDGOVITKEEFCEIFRAKDKTTGKLTCKKFKQRDG 60
QY 61 RRVKRAKKEIGILKXVKEPNILQVDFVTRKEVIFLELATGREVPMILDQGYSEER 120
DB 61 RRVKRAKKEIGILKXVKEPNILQVDFVTRKEVIFLELATGREVPMILDQGYSEER 120
QY 121 DTSNVRQVLEAVAYHSLKIYHRNKLKNTLYYRRLKSKXIVISPHLAKIENGLIKEP 180
DB 121 DTSNVRQVLEAVAYHSLKIYHRNKLKNTLYYRRLKSKXIVISPHLAKIENGLIKEP 180
QY 121 DTSNVRQVLEAVAYHSLKIYHRNKLKNTLYYRRLKSKXIVISPHLAKIENGLIKEP 180
DB 121 DTSNVRQVLEAVAYHSLKIYHRNKLKNTLYYRRLKSKXIVISPHLAKIENGLIKEP 180
QY 181 CGPEVTLAEVVGROGRPVDCWALGVIMYILSGNPPEVEEDDVENHDKLFRKI 240
DB 181 CGPEVTLAEVVGROGRPVDCWALGVIMYILSGNPPEVEEDDVENHDKLFRKI 240
QY 241 IAGDYFDSBYWDISQAADLVTRLMVEYBODRITAEBAISHWISGNAADKXIKQGV 300
DB 241 IAGDYFDSBYWDISQAADLVTRLMVEYBODRITAEBAISHWISGNAADKXIKQGV 300
QY 301 CAQIEKFPARAKKKAIVRTTLMKRLPAPQOSTAAQASATDTATPPAAGATLAAS 360
DB 301 CAQIEKFPARAKKKAIVRTTLMKRLPAPQOSTAAQASATDTATPPAAGATLAAS 360
QY 301 CAQIEKFPARAKKKAIVRTTLMKRLPAPQOSTAAQASATDTATPPAAGATLAAS 360
DB 301 CAQIEKFPARAKKKAIVRTTLMKRLPAPQOSTAAQASATDTATPPAAGATLAAS 360
QY 361 GATSAPEGDAARAASGNVAPADRATPATDGSATATGSGVTPADGSIPTATGSGVTP 420
DB 361 GATSAPEGDAARAASGNVAPADRATPATDGSATATGSGVTPADGSIPTATGSGVTP 420
QY 351 -----ADRSATPATDGSATPATDGSVTPADGSIPTATGSGVTP 389
DB 351 -----ADRSATPATDGSATPATDGSVTPADGSIPTATGSGVTP 389
QY 421 VTDRSATPATDGSATPATDGSVTPATGSGVTPATGSGVTPATGSGVTPATGSGVTP 480
DB 421 VTDRSATPATDGSATPATDGSVTPATGSGVTPATGSGVTPATGSGVTPATGSGVTP 480
QY 481 PSSKGEBAAGYAQESGREAS 501
DB 481 PSSKGEBAAGYAQESGREAS 501
QY 450 PSSKGEBAAGYAQESGREAS 470
DB 450 PSSKGEBAAGYAQESGREAS 470

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RESULT 10
AAM38987

```

ID AAM38987 standard; protein; 470 AA.
XX
XX AAM38987;
AC
XX 22-OCT-2001 (first entry)
DT
XX
XX Human polypeptide SEQ ID NO 2132.
DE
XX
XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
KM leukaemia.
XX
XX Homo sapiens.
OS
XX
XX MO200153312-A1.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 26-DEC-2000; 2000MO-US034263.
PF
XX
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa,
PI Zhou P, Goodrich R, Dmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AAI58143.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
FT
XX
XX Example 4; SEQ ID NO 2132; 10078bp; English.
PS
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AA42213) with noctropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 470 AA;
SQ
Query Match 92.7%; Score 2391.5; DB 4; Length 470;
Best Local Similarity 93.2%; Pred. No. 1e-172;
Matches 467; Conservative 1; Mismatches 2; Indels 31; Gaps 1;
QY 1 MPFGCVTLGDKKXNNPSEVTDRLDGOVITKEEFCEIFRAKDKTTGKLTCKKFKQRDG 60
DB 1 MPFGCVTLGDKKXNNPSEVTDRLDGOVITKEEFCEIFRAKDKTTGKLTCKKFKQRDG 60

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QY 61 RKTKAKAKNETGILKMTKHPNIILOVDVFTTRKRYFFIFLELATGRREVEFDIILDOGYYSER 120
DB 61 RKTKAKAKNETGILKMTKHPNIILOVDVFTTRKRYFFIFLELATGRREVEFDIILDOGYYSER 120
QY 121 DTSNVVQVLEAVAYLHSLKIVHRNKLKENLVYNNRLKNSKIVSDPHLAKLNGGLKEP 180
DB 121 DTSNVVQVLEAVAYLHSLKIVHRNKLKENLVYNNRLKNSKIVSDPHLAKLNGGLKEP 180
QY 181 CGTPEYLAPEVVGQRYPVDCWAGIVIMYILISGNPPFEYEEVEDYENHDKNLFKRI 240
DB 181 CGTPEYLAPEVVGQRYPVDCWAGIVIMYILISGNPPFEYEEVEDYENHDKNLFKRI 240
QY 241 LAGDYEPDSFYWDIDISQAADLVTRLMEVEDQRTTAEALSHWISGNAASDKNIKDGV 300
DB 241 LAGDYEPDSFYWDIDISQAADLVTRLMEVEDQRTTAEALSHWISGNAASDKNIKDGV 300
QY 301 CAQIEKMPARAKMKKAVVTTLMKRLAPBEGSSTAAQASATDTATPGG----- 350
DB 301 CAQIEKMPARAKMKKAVVTTLMKRLAPBEGSSTAAQASATDTATPGG----- 350
QY 361 GATAPBEGDAAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
DB 361 GATAPBEGDAAARAASDNVAPADRSATPATDGSATPATDGSVTPATDGSVTP 420
QY 421 VTDRSATPATDGRATPATTEESTVPTTOSAMLTAKAATPEPAAQDPSTAPGATGAP 480
DB 421 VTDRSATPATDGRATPATTEESTVPTTOSAMLTAKAATPEPAAQDPSTAPGATGAP 480
QY 481 PSSKGEBAAGYAQSOREEAS 501
DB 481 PSSKGEBAAGYAQSOREEAS 501
QY 450 PSSKGEBAAGYAQSOREEAS 470
DB 450 PSSKGEBAAGYAQSOREEAS 470

RESULT 11
AAB42348
ID AAB42348 standard; protein; 284 AA.
XX
AC AAB42348;
XX
DE Human ORFX ORF2112 polypeptide sequence SEQ ID NO:4224.
XX
XX Human: open reading frame; ORFX; detection: cytostatic; hepatotropic;
XX vulnary; antiparkinsonian; noctropic; neuroprotective;
XX anticonvulsant; osteopathic; antidiabetic; immunosuppressant; cardiant;
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
XX antiviral; dermatological; immunosuppressive; antiinflammatory;
XX antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
XX antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
XX cholesterol ester storage; systemic lupus erythematosus; infection;
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
XX bone damage; cartilage damage; antiinflammatory disease; coagulation;
XX thrombosis; contraceptive.
XX
XX Homo sapiens.
XX
XX OS
XX FN WO200058473-A2.
XX
XX PD 05-OCT-2000.
XX
XX PF 31-MAR-2000; 2000WO-US008621.
XX
XX PR 31-MAR-1999; 99US-0127607P.
XX
XX PR 02-APR-1999; 99US-0127636P.
XX
XX PR 05-APR-1999; 99US-0127728P.
XX
XX PR 30-MAR-2000; 2000US-00540763.
XX
XX (CURA-) CURAGEN CORP.
XX

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PI Shinkets RA, Leach W;
XX
XX MPI; 2000-602362/57.
DR N-PSDB; AAC76557.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 11; Page 3417-3418; 5507pp; English.
XX
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnary;
XX antiparkinsonian; osteopathic; neuroprotective; osteopathic;
XX anticonvulsant; antidiabetic; immunosuppressant; immunostimulant;
XX cardiac; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;
XX antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
XX sequences can be used for determining the presence of or predisposition
XX to, or preventing or treating pathological conditions associated with an
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX
XX proteins in gene therapy vectors. The proteins and nucleic acids may be
XX used to treat cancers, proliferative disorders, neurodegenerative
XX disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
XX diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
XX storage, systemic lupus erythematosus, severe combined immunodeficiency
XX (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
XX disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
XX cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
XX enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
XX
XX Sequence 284 AA;
XX
XX Query Match 54.4%; Score 1403.5; DB 3; Length 284;
XX Best Local Similarity 87.9%; Pred. No. 4.1e-98;
XX Matches 277; Conservative 1; Mismatches 6; Indels 31; Gaps 1;

QY 111 IIDOGYYSERDTSNVVQVLEAVAYLHSLKIVHRNKLKENLVYNNRLKNSKIVSDPHLA 170
DB 1 IIDOGYYSERDTSNVVQVLEAVAYLHSLKIVHRNKLKENLVYNNRLKNSKIVSDPHLA 60
QY 171 KLENGLIKPECPTEPYLAPEVVGQRYPVDCWAGIVIMYILISGNPPFEYEEVEDY 230
DB 61 KLENGLIKPECPTEPYLAPEVVGQRYPVDCWAGIVIMYILISGNPPFEYEEVEDY 120
QY 231 NHDKNLFRKILAGDYEPDSFYWDIDISQAADLVTRLMEVEDQRTTAEALSHWISGNA 290
DB 121 NHDKNLFRKILAGDYEPDSFYWDIDISQAADLVTRLMEVEDQRTTAEALSHWISGNA 180
QY 291 ASDKNIKDGVCAQIEKMPARAKMKKAVVTTLMKRLAPBEGSSTAAQASATDTATPGG 350
DB 181 ASDKNIKDGVCAQIEKMPARAKMKKAVVTTLMKRLAPBEGSSTAAQASATDTATPGG 240
QY 351 AGCATRAAASGATSPBEGDAAARAASDNVAPADRSATPATDGSATPATDGSITPATDSI 410
DB 241 -----ADRSATPATDGSATPATDGSITPATDSI 269
QY 411 TPATDGSVTPVTDRS 425
DB 270 TPATDGSVTPATDS 284

RESULT 12
AABUS2789
ID AABUS2789 standard; protein; 289 AA.
XX
XX AABUS2789;
XX
XX 14-APR-2003 (first entry)
XX
XX Human signal transduction-associated DKFZphb12_82e4 homologue #1.
XX

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XX Human; gene therapy; vaccine; disease treatment; detection.
OS Homo sapiens.
XX MO200112659-A2.
XX 22-FEB-2001.
XX 18-AUG-2000; 2000MO-IB001496.
XX 18-AUG-1999; 99US-0149499P.
XX 28-SEP-1999; 99US-0156503P.
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX Wiemann S;
XX MPI; 2001-327840/34.
XX Nucleic acids having the sequences of clones isolated from libraries of
XX different human tissues, useful in recombinant DNA methodologies.
XX Example III; Page 354; 1095pp; English.
XX This invention describes novel polynucleotides and polypeptides isolated
XX from human cDNA libraries which can be used for gene therapy or in
XX vaccines. The polynucleotides of the invention and antibodies encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate polypeptide expression. The products of the
XX invention may also be used to identify modulators of expression and
XX activity and to down regulate expression and activity. The antibodies of
XX the invention may also be used as diagnostic agents for detecting the
XX presence of polypeptides in samples. This sequence represents a homologue
XX of a polypeptide described in the disclosure of the invention
XX
SQ Sequence 289 AA;
Query Match 48.6%; Score 1255.5; DB 4; Length 289;
Best Local Similarity 86.4%; Pred. No. 7e-87;
Matches 254; Conservative 4; Mismatches 23; Indels 13; Gaps 2;
QY 216 GNDPFYEVEEDDYENHDKNLFKRIIAGDYEPDPSYWDISQAQDLVRLNEVEQDQRI 275
Db 1 GNDPFYEVEEDDYENHDKNLFKRIIAGDYEPDPSYWDISQAQDLVRLNEVEQDQRI 60
QY 276 TAEBAISHWISGNAASDKIKDVCQAQIEKFNPAKAKKAVVITLMRLAPQSSGA 335
Db 61 TAEBAISHWISGNAASDKIKDVCQAQIEKFNPAKAKKAVVITLMRLAPQSSGA 120
QY 336 AASASATDTATPGAGGATPAAASG-----ATSAPEGDAAPAKSDNVAPADRSAT 387
Db 121 A-----TSDATPGAGGAAVAAAAGAAPASGASATVGTGGDCAKSDNVAASDRSXT 175
QY 388 PATDGSATPATDGSVTPATDGSITPATDGSVTPVTRSATPATDGSATPATEESTVPTQ 447
Db 176 PATDGSATPATDGSVTPATDGSITPATDGSVTPVTRSATPATDGSATPATEESTVPTQ 235
QY 448 SSAMLATKAAATPEPMAQPDSTAPGATGQAPSSKGBEBAAGVQSGREBAS 501
Db 236 SSAPAPAKAAATPEPMAVACPSTALGATGQAPSSKGBEBAAGVQSGREBAS 289
RESULT 13
ABUS2790
ID ABUS2790 standard; protein; 187 AA.
XX
AC ABUS2790;
XX
XX 14-APR-2003 (first entry)
XX Human signal transduction-associated DKFZphf02_82e4 homologue #2.
XX Human; gene therapy; vaccine; disease treatment; detection.

XX Homo sapiens.
OS Homo sapiens.
XX MO200112659-A2.
XX 22-FEB-2001.
XX 18-AUG-2000; 2000MO-IB001496.
XX 18-AUG-1999; 99US-0149499P.
XX 28-SEP-1999; 99US-0156503P.
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX Wiemann S;
XX MPI; 2001-327840/34.
XX Nucleic acids having the sequences of clones isolated from libraries of
XX different human tissues, useful in recombinant DNA methodologies.
XX Example III; Page 354; 1095pp; English.
XX This invention describes novel polynucleotides and polypeptides isolated
XX from human cDNA libraries which can be used for gene therapy or in
XX vaccines. The polynucleotides of the invention and antibodies encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate polypeptide expression. The products of the
XX invention may also be used to identify modulators of expression and
XX activity and to down regulate expression and activity. The antibodies of
XX the invention may also be used as diagnostic agents for detecting the
XX presence of polypeptides in samples. This sequence represents a homologue
XX of a polypeptide described in the disclosure of the invention
XX
SQ Sequence 187 AA;
Query Match 37.9%; Score 978; DB 4; Length 187;
Best Local Similarity 99.5%; Pred. No. 4.3e-66;
Matches 186; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFGCVTLGDKKNYNOSEVTDYDLGQVYKTEBFCEIFPAKQTKTKLTKCKFKORDG 60
Db 1 MPFGCVTLGDKKNYNOSEVTDYDLGQVYKTEBFCEIFPAKQTKTKLTKCKFKORDG 60
QY 61 RKVRKAKNEIGILKWKVHNILQLVDVFTYRKEVFFLELATGREVFDMILDOGYYSR 120
Db 61 RKVRKAKNEIGILKWKVHNILQLVDVFTYRKEVFFLELATGREVFDMILDOGYYSR 120
QY 121 DTSNVAVQVLEAVAYLHSLKIVHNLKLENIYYNRLKNSKIYISDFHLAKLENGLIKPEP 180
Db 121 DTSNVAVQVLEAVAYLHSLKIVHNLKLENIYYNRLKNSKIYISDFHLAKLENGLIKPEP 180
QY 181 CGTPEYL 187
Db 181 CGTPEYL 187
RESULT 14
AAU87207
ID AAU87207 standard; protein; 204 AA.
XX
AC AAU87207;
XX
XX 05-JUN-2002 (first entry)
XX Novel central nervous system protein #117.
XX
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; ischemia; angiodysplasia;
XX nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
XX acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
XX adenocarcinoma; reproductive system disorder; testicular feminisation;

PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232403P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237040P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249266P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250316P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251889P.
PR 08-DEC-2000; 2000US-0251990P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-465460/50.
DR N-PSDB; AAS27184.
XX
XX Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
PS Claim 1; SEQ ID NO 832; 880bp; English.
XX
XX The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU1059-
CC AAU1683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX
Query Match 33.0%; Score 852; DB 4; Length 219;
Best Local Similarity 72.6%; Pred No. 1.9e-56;
Matches 172; Conservative 5; Mismatches 20; Indels 40; Gaps 2;
QY 186 YLAPEVVGQRGRYPVCAIVIMYLLSGNPPYEVEEDDYENHDKNLFKILAGDY 245
DB 14 FVAPEVVGQRGRYPVCAIVIMYLLSGNPPYEVEEDDYENHDKNLFKILAGDY 73
QY 246 EPDSEPYWDDISQAADLVTRLMVEVDODRTAEKAIISHWISGNAASDKNIDGVCAGIE 305
DB 74 XEDSPYWDIDISQAADLVTRLMVEVDODRTAEKAIISHWISGNAASDKNIDGVCAGIE 133
QY 306 KNFAPAKKKKAVRVTIMRLAPROSSAAQASATDTAPGAAGGATAAAGANSA 365
DB 134 KNFAPAKKKKAVRVTIMRLAPROSSAAQASATDTAPGAAGGATAAAGANSA 178
QY 366 PEGDAARAASDNVAADRSATPATDGSATPATDGSATPATD-----GSITPA 413
DB 179 -----ADKPCPPQPMQEVFPQPLAIVSPQPMQASXKPLMGSVTPA 219
Search completed: April 23, 2004, 15:48:15
Job time : 62 secs

POEMED 11042159
REFERENCE 3
AUTHORS Shizata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komori, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3692)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koya, S., Kirihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shizata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 220-0045, Japan (E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Query Match 54.2%; Score 1691.8; DB 11; Length 3692;

Best Local Similarity 77.9%; Pred. No. 2,99-220;
Matches 2422; Conservative 0; Mismatches 514; Indels 173; Gaps 25;
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288 CAAGCTGCACACTGCAAGAGTTCAGAAAGCGGACGCGCGAGAGTGGGAAAGCTGC 347
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648 -CACTGCTAGCTAGAAATGGCTCATCAAGAGCCCTGTGGGACCCCGAGATCTGCTG 706
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707 CACCAGAGAGTGTAGAGCGCGAGCGGATGAGACCGCTGTGAGCTGTGAGCTGTGAG 766
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FEATURES	source
1. .1201	
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DEFINITION	CSODF009Y013 3-PRIME, mRNA sequence.
ACCESSION	EX440618
VERSION	EX440618.1 GI:30771860
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1201)
TITLE	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished (2001)
	Contact: Genoscope
	Genoscope - Centre National de Sequencage
	BP 191 91006 EVRY cedex - France
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
	Library was constructed by Life Technologies, a division of
	Invitrogen. This sequence belongs to sequence cluster 1934.r For
	more information about this cluster, see
	http://www.genoscope.cns.fr/
	cgl-bin/cluster.cgi?seq=CSODF009AH07ND1&cluster=1934.r. Contact :
	Feng Liang Email : fliang@life.techn.com URL :
	http://fulllength.invitrogen.com/Invitrogen Corporation 1600
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ORIGIN

	Query Match	Similarity	DB 13;	Score	951;	Length	1201;	
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OY	1989	TTCCTTTGGGAATGTGCTCTAAGGAATCTCAGGGGGGCTCCGAGCTCCTTCCCTCCC	2048					
Dp	1041	TTCCCTTKTGATGTCTCTTAAGGAATCTCAGGGGGGCTCCGCTCTCTCTTCCCTTCCC	982					
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Dp	981	TTCTTGCCCTCACCATTTCCCTTAGAGAGGCCCTGCAGAGTCCCACTCTTCCAGGCCCTAA	922					
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Dp	921	ACTTGGGGGGGCTTSCCTGAGAGTGTCCTCCACGAGAGGCCCTGTGACGGGTCTTAAG	862					
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Dp	861	CTCTCTGCACATGAAGTGTGTGCTGTGTGTGTGGGCTGTCTTAGAGACAATACAGGC	802					
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Dp	801	TGGTATAGAGATNGCAGAAAGGTAAGGGGAGTAATGTTTAAGTCCAGACTTGGGCATAGGCT	742					
OY	2289	AAGGATATACGTCTCACTAGCTGTGAGAGTCTCCAGAGAGTGGAGAGAAATGATAGAGAGCA	2348					
Dp	741	AAGGATATACGTCTCACTAGCTGTGAGAGTCTCCAGAGAGTGGAGAGAAATGATAGAGAGCA	682					
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Dp	681	AAAAGCTTCATTTTGTCTCTCTTAAGACCCTGTTATTTGTGTATTTCTGCTTTCCA	622					
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Dp	621	AGTCCTGCAGTGGGCTGCCCTGTACCCCTGAACCTCATAGAGCCTTAAGGGAAMAAAAA	562					
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VERSION	BX460352		
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AUTHORS	Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 1027)		
JOURNAL	Li, W.B., Gruber, C., Jeasee, J. and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization Unpublished (2001)		
FEATURES	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seque@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1934.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DF013BB01QPLcluster=1934.r. Contact : Feng Liang Email : fliang@lifetech.com URL : Corporation 1600 http://fulllength.invitrogen.com/ Invitrogen Genoscope Faraday Avenue Genoscope sequence ID : CS0DF013BB01QPL. location/Qualifiers		
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ORIGIN			
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DEFINITION	AL568260 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone		
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VERSION	AL568260		
KEYWORDS	AL568260.2 GI:31291103		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Bukacinski, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On Feb 16, 2001 this sequence version replaced gi:12922422.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 19191006 Evry cedex - France		

Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1934.r For more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF032CE06NP1&cluster=1934.r)
[cgi-bin/cluster.cgi?seq=CS0DF032CE06NP1&cluster=1934.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF032CE06NP1&cluster=1934.r). Contact :

Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>

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FEATURES

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enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the PCMVSPORT 6
vector. Library was not normalized."
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ORIGIN

Query Match

29.8%; Score 932.4; DB 9; Length 1201;

Best Local Similarity 91.5%; Pred. No. 4.1e-117; Mismatches 66; Indels 3; Gaps 3;

Matches 987; Conservative 23; Mismatches 66; Indels 3; Gaps 3;

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DB 1081 CAGCCSCCACCACCCCTSVAKANCTTGTGTTTTTTTTTCTAGTTCACMATTTCT 1022
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DB 1021 KTHCYTKTGTGATGKCTTARGGATATCTCAAGGAGGCTCTGCTCT-CATCCCTTCCCT 963
QY 2050 TCTTGCTCACTATCCCTTCAAGGAGGCTCTGAGGCTCCACACTCTCCAGGCTTAA 2109
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QY 2110 CTGAGGAGGCTTGCCTTCAAGGAGGCTCTGAGGAGGCTCTGAGGCTTAA 2169
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QY 2170 TCCTGCATGAGAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2229
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QY 2470 AATTAGAGCTGTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2529
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QY 2530 AGCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2589
DB 482 AGCCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 423
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ORIGIN

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QY 2590 TAGATGCCACCTCTTCAATCTTCAGCCCAAGTCTCTTCCACCTTAGGGGCTTGTCTG 2649
DB 422 TAGATGCCACCTCTTCAATCTTCAGCCCAAGTCTCTTCCACCTTAGGGGCTTGTCTG 363
QY 2650 CATGGCAATATCTATATATGTGATTTTGGAGTTTGGCCCTTTTACAGGGGAGATTTTGTG 2709
DB 362 CATGGCAATATCTATATATGTGATTTTGGAGTTTGGCCCTTTTACAGGGGAGATTTTGTG 303
QY 2710 TCAGTTCACATGAATATGAAGAGAACTCCCTCTTCTTCAAGCTCACTTCTTACAGAG 2769
DB 302 TCAGTTCACATGAATATGAAGAGAACTCCCTCTTCTTCAAGCTCACTTCTTACAGAG 243
QY 2770 CCGAGTGTCTCAGAGCCACATTTAGTGTCTTTTCTGAGATGAGAGAGGTTTAAAC 2829
DB 242 CCGAGTGTCTCAGAGCCACATTTAGTGTCTTTTCTGAGATGAGAGAGGTTTAAAC 183
QY 2830 TCCCAAGTTTCTGAGGAGGCTCTTCAAGAGTGTCTTGTCAAGACCTTACAGAGCT 2889
DB 182 TCCCAAGTTTCTGAGGAGGCTCTTCAAGAGTGTCTTGTCAAGACCTTACAGAGCT 123
QY 2890 GGATTA-GGAGAGCCATTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2948
DB 122 GGATTA-GGAGAGCCACATTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64
QY 2949 CTCCCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3007
DB 63 CCCCWCATCTCTGTGANTCTNCTNNTGTTTGAAGATCATAGATTAATTAATTAATTAAC 5
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RESULT 10
BX461112 1201 bp mRNA linear EST 22-MAY-2003
LOCUS BX461112 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF022YJ18 5-PRIME, mRNA sequence.
ACCESSION BX461112
VERSION BX461112.1 GI:31035270
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1934.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF022DF09QPI&cluster=1934.r. Contact :
Feng Liang Email : liang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue Genoscope sequence ID : CS0DF022DF09QPI.
Location/Qualifiers
1.1201
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the PCMVSPORT 6
vector. Library was not normalized."
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Query Match 29.2%; Score 911.4; DB 13; Length 1201;
 Best Local Similarity 97.7%; Pred. No. 2,9e-114;
 Matches 931; Conservative 12; Mismatches 8; Indels 2; Gaps 2;

98 CCGCGCTGCTGGAGCGGATTTTCGCCCGCTGCCGAGACCTTCGGGCGCCCGCTGAGC 157
 Db CCGCGGATCTTCGGAGCGGATTTTCGCCCGCTGCCGAGACCTTCGGGCGCCCGCTGAGC 119
 60 CCGCGGATCTTCGGAGCGGATTTTCGCCCGCTGCCGAGACCTTCGGGCGCCCGCTGAGC 119
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 Db CCGCGGATCTTCGCCCGCTGAGC 179
 120 CCGCGGATCTTCGCCCGCTGAGC 179
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 180 TTGGGATGTTGAGCTCTGGGCGAGAGAGACTTAACCGCCATCGAGGATGATGACA 239
 QY GATATGATTTGGGAGAGGTCATCAAGCTGAGAGGTTTGTAAATCTTCGGGCGAGG 337
 Db GATATGATTTGGGAGAGGTCATCAAGCTGAGAGGTTTGTAAATCTTCGGGCGAGG 299
 240 GATATGATTTGGGAGAGGTCATCAAGCTGAGAGGTTTGTAAATCTTCGGGCGAGG 299
 QY ACAAGAGCAGCGGAGAGGTCGACCTGCGAAGAGTTCCAGAGCGGAGCGGCGAGG 397
 Db ACAAGAGCAGCGGAGAGGTCGACCTGCGAAGAGTTCCAGAGCGGAGCGGCGAGG 359
 300 ACAAGAGCAGCGGAGAGGTCGACCTGCGAAGAGTTCCAGAGCGGAGCGGCGAGG 359
 QY TGCGGAAAGCTGCGAGAGAGATAGGATCTTCAGATGTTGAGAGATCCCAATCC 457
 Db TGCGGAAAGCTGCGAGAGAGATAGGATCTTCAGATGTTGAGAGATCCCAATCC 419
 360 TGCGGAAAGCTGCGAGAGAGATAGGATCTTCAGATGTTGAGAGATCCCAATCC 419
 QY TACAGCTGTTGATGTTGTTGAGACCGCGAGAGATCTTATCTTCCTGGAGCTGAGCA 517
 Db TACAGCTGTTGATGTTGTTGAGACCGCGAGAGATCTTATCTTCCTGGAGCTGAGCA 479
 420 TACAGCTGTTGATGTTGTTGAGACCGCGAGAGATCTTATCTTCCTGGAGCTGAGCA 479
 QY CGGAGAGGAGGAGGTTGATGATCTGACACCGGCTACTACTCTCGAGCGAGACACAA 577
 Db CGGAGAGGAGGAGGTTGATGATCTGACACCGGCTACTACTCTCGAGCGAGACACAA 539
 480 CGGAGAGGAGGAGGTTGATGATCTGACACCGGCTACTACTCTCGAGCGAGACACAA 539
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 Db GCACAGTGTGACGAGAGTCTCTGAGAGCGGCTGCTATTTGCACTCACTCAAGATTCGTC 599
 540 GCACAGTGTGACGAGAGTCTCTGAGAGCGGCTGCTATTTGCACTCACTCAAGATTCGTC 599
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 600 ACAGGATCTCAAGCTGAGAGACCTGTTTCTCAACACCGGCTGAGAGATTCGAGATTG 659
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 660 TCATCAGTGAATCTTCATCTGGCTAAGTAAAGATGAGCTCATCAGAGAGCCCTGAGG 719
 QY CCCCCGAGATCTGAGCCCGAGAGGTTGAGCGCGGATGAGAGCCCTGAGGACT 817
 Db CCCCCGAGATCTGAGCCCGAGAGGTTGAGCGCGGATGAGAGCCCTGAGGACT 779
 720 CCCCCGAGATCTGAGCCCGAGAGGTTGAGCGCGGATGAGAGCCCTGAGGACT 779
 QY GCTGGGCGATGAGATCATCATCTGCTTTCAGGCAATCCATCTTCATGAGG 877
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 900 GTGATGATGATTTGATCTTCATTA-TTGGGATGATTTTGGAGGAGCGGAGAGAGCTG 959
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RESULT 11
 LOCUS BX460131 1201 bp mRNA linear EST 22-MAY-2003
 DEFINITION BX460131 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone

ACCESSION CS0DF011Y20 5-PRIME, mRNA sequence.

VERSION BX460131 GI:31023203

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1201)

Li W.B., Gruber C., Jessee J., and Polayes D.

Full-length cDNA libraries and normalization

Unpublished (2001)

COMMENT

Genoscope - Centre National de Sequencage

Genoscope BP 191 91006 Evry cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1934.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DF011Y20&cluster=1934.r. Contact:

Feng Liang Email: fliang@lifetech.com URL: Corporation 1600

Parade Avenue Genoscope sequence ID: CS0DF011Y20PL.

Location/Qualifiers

1..1201

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/db_xref="taxon:9606"

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/dev_stage="fetal"

/clone_1ib="Homo sapiens FETAL BRAIN"

/note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 29.0%; Score 906.8; DB 13; Length 1201;
 Best Local Similarity 98.1%; Pred. No. 1.2e-113;
 Matches 942; Conservative 6; Mismatches 8; Indels 4; Gaps 3;

63 CTAGCGGAGCGGCTGATCTGCGCGCGCTGCTGCCCGCTGCGAGCGGATTTTCG 122
 Db CTAGCGGAGCGGCTGATCTGCGCGCGCTGCTGCCCGCGCTGCGAGCGGATTTTCG 129
 70 CTAGCGGAGCGGCTGATCTGCGCGCGCTGCTGCCCGCGCTGCGAGCGGATTTTCG 129
 QY CCGCGCTCCCCGAGAGCCCTCGGCGCGCGCTGAGCGCGGATCACTTCCTCGTGAAC 182
 Db CCGCGCTCCCCGAGAGCCCTCGGCGCGCGCTGAGCGCGGATCACTTCCTCGTGAAC 189
 130 CCGCGCTCCCCGAGAGCCCTCGGCGCGCGCTGAGCGCGGATCACTTCCTCGTGAAC 189
 QY AACCGGCGCTGAGGTTAGAGCTGAGCAATGCGGTTGGGTGTGATCTGCGGCGACA 242
 Db AACCGGCGCTGAGGTTAGAGCTGAGCAATGCGGTTGGGTGTGATCTGCGGCGACA 249
 190 AACCGGCGCTGAGGTTAGAGCTGAGCAATGCGGTTGGGTGTGATCTGCGGCGACA 249
 QY GAAGAATTAACACAGCATCGAGGTGATGACAGATATGATTTGGAGAGGTCTATCAA 302
 Db GAAGAATTAACACAGCATCGAGGTGATGACAGATATGATTTGGAGAGGTCTATCAA 309
 243 GAAGAATTAACACAGCATCGAGGTGATGACAGATATGATTTGGAGAGGTCTATCAA 302
 250 GAAGAATTAACACAGCATCGAGGTGATGACAGATATGATTTGGAGAGGTCTATCAA 309
 QY GACTGAGAGGTTTGTGAAATCTTCGCGGCGAGAGCAAGAGCAAGAGTGTGACAC 362
 Db GACTGAGAGGTTTGTGAAATCTTCGCGGCGAGAGCAAGAGCAAGAGTGTGACAC 369
 310 GACTGAGAGGTTTGTGAAATCTTCGCGGCGAGAGCAAGAGCAAGAGTGTGACAC 369
 QY CTGCAAGAGTTTCCAGAGGCGGAGCGGCGAGAGGCGGAAAGCTGCCAAGACAGAT 422
 Db CTGCAAGAGTTTCCAGAGGCGGAGCGGCGAGAGGCGGAAAGCTGCCAAGACAGAT 429
 370 CTGCAAGAGTTTCCAGAGGCGGAGCGGCGAGAGGCGGAAAGCTGCCAAGACAGAT 429
 QY AGGCATCTCAAGATGTGAGATCCCAACATCTTACAGCTGTGTGTGATGAG 482
 Db AGGCATCTCAAGATGTGAGATCCCAACATCTTACAGCTGTGTGTGATGAG 489
 430 AGGCATCTCAAGATGTGAGATCCCAACATCTTACAGCTGTGTGTGATGAG 489
 QY CCGCAAGAGTACTTATCTTCCTGAGAGCTGCGACCGGAGGAGGTGTTTACTGAT 542
 Db CCGCAAGAGTACTTATCTTCCTGAGAGCTGCGACCGGAGGAGGTGTTTACTGAT 542


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Db      490 CGGACAGAGTACTTATCTTCTGAGTGGCCACGGGAGGGGGTGTGACTGGAT 549
Qy      543 CCTGACACGAGCTACTACTCGGAGGAGACACAAGCAACGTGTACCGCAAGTCTTGA 602
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Qy      603 GGCCTGAGCTATTTGCACTCACTCAAGATCTGACAGAGAACTCTCAAGCTGAGAACT 662
Db      610 GGCCTGAGCTATTTGCACTCACTCAAGATCTGACAGAGAACTCTCAAGCTGAGAACT 669
Qy      663 GGTATTACTCAACCGGCTAAGAACTCAAGATTTGATCATAGTACTTCCATCTGGCTAA 722
Db      670 GGTATTACTCAACCGGCTAAGAACTCAAGATTTGATCATAGTACTTCCATCTGGCTAA 729
Qy      723 GGTAGAAATGGCTCATAGAGAGCCCTGTGGGACCCCGGATCTGGGCCGAGAGT 782
Db      730 GGTAGAAATGGCTCATAGAGAGCCCTGTGGGACCCCGGATCTGGGCCGAGAGT 789
Qy      783 GGTAGAGCCGAGAGGCTATGACAGCCCTGTGGAGTCTGGGCAATTGATCATATGTA 842
Db      790 GGTAGAGCCGAGAGGCTATGACAGCCCTGTGGAGTCTGGGCAATTGATCATATGTA 849
Qy      843 CATCTGCTTTCAGGCAATCCACCTTTCTATAGAGAGGTGGAAGATGATTATGAGAA 902
Db      850 CATCTGCTTTCAGGCAATCCACCTTTCTATAGAGAGGTGGAAGATGATTATGAG-A 908
Qy      903 CATGATAGAGTCTTCTTCCGCAAGATCTGGCTGTGATCTATGATTGATCTTCCATA 962
Db      909 KCATGATAGAGTCTTCTTCCGCAAGATCTGGCTGTGATCTATGATTGATCTTCCATA 968
Qy      963 TTGGAGTATATTTCGACAGAGCAAGCAAGACTGTGCAAGAGCTGATGAGAGAGACA 1022
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RESULT 12
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LOCUS      BX425447      Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION      BX425447
ACCESSION      BX425447
VERSION      BX425447
KEYWORDS      BX425447.1 GI:30782455
SOURCE      EST.
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Li, W.B., Gruber, C., Tesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1934.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL08B014ZE06R1&cluster=1934.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CL08B014ZE06R1.
Location/Qualifiers
1..964
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL08B014ZE06"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed

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```

FEATURES
source

```

ORIGIN

with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

Query Match 28.3%; Score 901.8; DB 13; Length 964;
 Best Local Similarity 97.6%; Freq. No. 6.2e-113;
 Matches 909; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

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Qy      26 CCGTGCCGCGCAGAGCGCTGCGCATCTGAGAGGTGCTGACAGCGGAGCGGCTGCATCTG 85
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Qy      86 CGCCGCGTCCGCCCGCGTCTGAGAGCGGATCTCCGCGTCCCGAGAGCCCTCGAG 145
Db      94 CGCCGCGTCCGCCCGCGTCTGAGAGCGGATCTCCGCGTCCCGAGAGCCCTCGAG 153
Qy      146 GCCCGCGTGAAGCCCGGATCACTTCTCTCTGTGACCAACCGGCGCTGAGAGT 205
Db      154 GCCCGCGTGAAGCCCGGATCACTTCTCTCTGTGACCAACCGGCGCTGAGAGT 213
Qy      206 TGGCATGCCGCTTGGGTGTGATCTTGGGCGCAAGAAAGATTAACCGGCAATCG 265
Db      214 TGGCAATGCCGCTTGGGTGTGATCTTGGGCGCAAGAAAGATTAACCGGCAATCG 273
Qy      266 AGGTGATGACAGATATGATTTGGGACAGGTCTCAAGACTGAGAGTGTGAAATCT 325
Db      274 AGGTGATGACAGATATGATTTGGGACAGGTCTCAAGACTGAGAGTGTGAAATCT 333
Qy      326 TCCGGGCGCAAGAGCAGACGACAGAGAGCTGACACTGCAAGAAATTCCAGAGCGG 385
Db      334 TCCGGGCGCAAGAGCAGACGACAGAGAGCTGACACTGCAAGAAATTCCAGAGCGG 393
Qy      386 ACCGCGCGAAGGTGCGGAAAGCTGCCAAGACAGATATGACATCTCAAGATGTGAGC 445
Db      394 ACCGCGCGAAGGTGCGGAAAGCTGCCAAGACAGATATGACATCTCAAGATGTGAGC 453
Qy      446 ATCCCAATCTCTCAAGCTGTGATGTGTTGACCCGCAAGAGTCTTATCTTCC 505
Db      454 ATCCCAATCTCTCAAGCTGTGATGTGTTGACCCGCAAGAGTCTTATCTTCC 513
Qy      506 TGGAGCTGCGCAGCGGAGGAGGTGTTGATCTGATCTCTGACAGGCTACTACTCG 565
Db      514 TGGAGCTGCGCAGCGGAGGAGGTGTTGATCTGATCTCTGACAGGCTACTACTCG 573
Qy      566 AGCAGACACAGAGCAAGTGTACCGCAAGTCTCTGAGGCGGCTATTTGACTCTAC 625
Db      574 AGCAGACACAGAGCAAGTGTACCGCAAGTCTCTGAGGCGGCTATTTGACTCTAC 633
Qy      626 TCAAGATCTGACAGAGATCTCAAGTGTGAGAACTGTGTTCTACACCGGCTGAGA 685
Db      634 TCAAGATCTGACAGAGATCTCAAGTGTGAGAACTGTGTTCTACACCGGCTGAGA 693
Qy      686 ACTGAGATTTGATGATGATGATCTCATGCTGCTGATAGTAAAGTGGCTCATCAAG 745
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Db      754 AGCCTGTGGAGACCCCGATATCTGCCCCAGAGGTGTAGGCGCGCAGCGGATGAGC 813
Qy      806 GCCCTGTGAGACTGTGGGCAATTTGAGTCAATGATCAATCTGCTTTCAGGCAATCAC 865
Db      814 GCCCTGTGAGACTGTGGGCAATTTGAGTCAATGATCAATCTGCTTTCAGGCAATCAC 873
Qy      866 CTTTCTATGAGAGAGTGAAGATGATATATGAGAACATATTAAGAAATCTCTCGCA 925
Db      874 CTTTCTATGAGAGAGTGAAGATATATATGAGAACATATTAAGAAATCTCTCGCA 933
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/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

```

ORIGIN
Query Match      28.0%; Score 875.4; DB 13; Length 955;
Best Local Similarity 96.5%; Pred. No. 2.4e-109;
Matches 864; Conservative 25; Mismatches 6; Indels 0; Gaps 0;

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QY 112 GCGGATTTCGCCCGCGCTGCGAGCCCTGCGCGCCGCTGCGAGCCGCGCATCTTCC 171
DB 121 GCGGATTTCGCCCGCGCTGCGAGCCCTGCGCGCCGCTGCGAGCCGCGCATCTTCC 180
QY 172 TCCCTGTGACCAACCGCGCTGAGTTGAGCTTGGCAATGCCGTTGGTGTGTACT 231
DB 181 TCCCTGTGACCAACCGCGCTGAGTTGAGCTTGGCAATGCCGTTGGTGTGTACT 240
QY 232 CTGGGCGCAAGAGAACTATTAACCAAGCATCGAGAGTGAATGATATGATTGGGA 291
DB 241 CTGGGCGCAAGAGAACTATTAACCAAGCATCGAGAGTGAATGATATGATTGGGA 300
QY 292 CAGGTCATCAAGACTGAGAGGTTTGTGAATCTTCCGCGCCAGAGCAAGACGACG 351
DB 301 CAGGTCATCAAGACTGAGAGGTTTGTGAATCTTCCGCGCCAGAGCAAGACGACG 360
QY 352 AAGCTGCAACCTGCAAGAGTTTCCAGAGCGGAGCGCGCAAGGTGCGGAAACCTGCC 411
DB 361 AAGCTGCAACCTGCAAGAGTTTCCAGAGCGGAGCGCGCAAGGTGCGGAAACCTGCC 420
QY 412 AAGAAAGAAATGAGCTCTCAAGATGAGAGCAATCCCAATCCTCAGCTGTGTAT 471
DB 421 AAGAAAGAAATGAGCTCTCAAGATGAGAGCAATCCCAATCCTCAGCTGTGTAT 480
QY 472 GGTGTTGTAACCGCAAGAGTACTTATCTTCTGAGAGCTGGCAAGCGGAGAGGTG 531
DB 481 GGTGTTGTAACCGCAAGAGTACTTATCTTCTGAGAGCTGGCAAGCGGAGAGGTG 540
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DB 661 CTGAGAACCTGTTTACTAACAACCGGCTGAAGAACTCGAAGTTGTCTCATGTA 720
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DB 721 CATCTGCTAAGCTAGAAAATGCTCATCAAGAGACCTGTGGGACCCCGAGATCTG 780
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QY 832 GTCATATGATACCTCTGCTTACGAGCATCCACTTTGATGAGAGAGGTGGAAGAGT 891
DB 841 GTCATATGATACCTCTGCTTACGAGCATCCACTTTGATGAGAGAGGTGGAAGAGT 900
QY 892 GATTATGAGAACCATTAAGATCTCTCCGCAAGATCCTGGCTGTACTATG 946
DB 901 AATTATGAGAACCATTAAGATCTCTCCGCAAGATCCTGGCTGTACTATG 955

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RESULT 15
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LOCUS BX423239 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF003YA22 3-PRIME, mRNA sequence.
ACCESSION BX423239
VERSION BX423239.1 GI:30766248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, D., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1934.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AF001ZE12NP1&cluster=1934.r. Contact :
Peng Liang Email: filiang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AF001ZE12NP1.
Location/Qualifiers

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FEATURES

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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dt) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

```

ORIGIN

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Query Match      27.8%; Score 867.6; DB 13; Length 1201;
Best Local Similarity 89.2%; Pred. No. 2.5e-108;
Matches 928; Conservative 17; Mismatches 92; Indels 3; Gaps 3;

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2056 CTCACATCTCCCTC-AGGCAAGCGCTGACAGTCCCACTCTCCAGGCGCTTAACTTGG 2114

978 CKACCAATCCCTGAGAGCGGCGCTGCAKCCCACTCTCCAGGCGCTTAACTTGG 919

2115 GCGGCTTGGCCCTGAGAGCTGATCTTCCAGAGGAGCGCTTCAAGCGTCTTAACTTGG 2174

918 GCGGCTTGGCCCTGAGAGCTGATCTTCCAGAGGAGCGCTTCAAGCGTCTTAACTTGG 859

2175 CACATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2234

858 CACATGAAGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 799

2235 AGAGAGTGAAGAAAGTGAAGGAGTATGTTAAGTCAAGCTTGGCATGAGTGAAGGAT 2294

798 AGAGAGTGAAGAAAGTGAAGGAGTATGTTAAGTCAAGCTTGGCATGAGTGAAGGAT 739

2295 ACTGCTACTAGCTGT 2354

738 ACTGCTACTAGCTGT 679

QY	301	AAGCTGAGGAGGATTTTGTGAAATTTCTCCGGGCCAAGGACAAGACGACGACGCTCAC	360
Db	301	AAGCTGAGGAGGATTTTGTGAAATTTCTCCGGGCCAAGGACAAGACGACGACGCTCAC	360
QY	361	ACCTGCAAGAAGTTCAGAAAGCGGGAAGCGCGCAAGGTGCGGAAAGCTGCCAAGACGAG	420
Db	361	ACCTGCAAGAAGTTCAGAAAGCGGGAAGCGCGCGCAAGGTGCGGAAAGCTGCCAAGACGAG	420
QY	421	ATAGGCATCCTCAAGATGATGAGACATCCCAATCCTCAGCTGTGAGATGTGTGTG	480
Db	421	ATAGGCATCCTCAAGATGATGAGACATCCCAATCCTCAGCTGTGAGATGTGTGTG	480
QY	481	ACCCGCAAGGAGTACTTTATCTCTCTGGAAGCTGGCCAGGCGGGAAGAGGTGTGACTCG	540
Db	481	ACCCGCAAGGAGTACTTTATCTCTCTGGAAGCTGGCCAGGCGGGAAGAGGTGTGACTCG	540
QY	541	ATCTGAGCAGAGGCGTACTACTCGGAGGAGACACAAGCAACGTGATACGGCAATCCTG	600
Db	541	ATCTGAGCAGAGGCGTACTACTCGGAGGAGACACAAGCAACGTGATACGGCAATCCTG	600
QY	601	GAGGCGGTGCGCTATTTTGCACTCACTCAAGATCGTGACAAGAAATCTCAAGCTGAGAAC	660
Db	601	GAGGCGGTGCGCTATTTTGCACTCACTCAAGATCGTGACAAGAAATCTCAAGCTGAGAAC	660
QY	661	CTGCTTTTACTCAACCCGGCTGAGAACTCGAAGATTGTCACTAGTGAATCTTCATCTGACT	720
Db	661	CTGCTTTTACTCAACCCGGCTGAGAACTCGAAGATTGTCACTAGTGAATCTTCATCTGACT	720
QY	721	AAGCTAAGAAATGCGCTTCATCAAGAGCGCTGTGGAGACCCCGAGTATCTGGCCCCAGAG	780
Db	721	AAGCTAAGAAATGCGCTTCATCAAGAGCGCTGTGGAGACCCCGAGTATCTGGCCCCAGAG	780
QY	781	GTGGTAGGCGCGGACGGATGAGAGCGCTGTGACATGCTGGGACCATGGAGTCAATCATG	840
Db	781	GTGGTAGGCGCGGACGGATGAGAGCGCTGTGACATGCTGGGACCATGGAGTCAATCATG	840
QY	841	TACATCCTGCTTTGAGGCAATCCAATCTTCTATGAGAGGTGAGAAAGATGATTAAG	900
Db	841	TACATCCTGCTTTGAGGCAATCCAATCTTCTATGAGAGGTGAGAAAGATGATTAAG	900
QY	901	AACCATGATTAAGAAATCTTCTCCGCAAGATCTGGCTGCTGACTTATGATTTGACTCTCCA	960
Db	901	AACCATGATTAAGAAATCTTCTCCGCAAGATCTGGCTGCTGACTTATGATTTGACTCTCCA	960
QY	961	TATTGGGATGATTTTGGCAGGACGCAAAACCTGGTCAACAAGCTGATGGAAGTGGAG	1020
Db	961	TATTGGGATGATTTTGGCAGGACGCAAAACCTGGTCAACAAGCTGATGGAAGTGGAG	1020
QY	1021	CAAGACCAAGCGGATCACTGCAAGAAAGGCGCATCTCCCATGATGAGATTTCTGGCAATGCT	1080
Db	1021	CAAGACCAAGCGGATCACTGCAAGAAAGGCGCATCTCCCATGATGAGATTTCTGGCAATGCT	1080
QY	1081	GCTTCTGATTAAGAACATCAAGAGATGTGTCTGTGCCAGATTGAAAGAACTTTGCCAGG	1140
Db	1081	GCTTCTGATTAAGAACATCAAGAGATGTGTCTGTGCCAGATTGAAAGAACTTTGCCAGG	1140
QY	1141	GCCAAGTGGAAAGAAAGGCTGTCCGAGTGACCACTCTCAAGAAACGAGCTCCGGGACACAGAG	1200
Db	1141	GCCAAGTGGAAAGAAAGGCTGTCCGAGTGACCACTCTCAAGAAACGAGCTCCGGGACACAGAG	1200
QY	1201	CAGTCCAGCAAGGCTGCAAGCCAGTCCGAGCTCAGCAACAGACCTGCCACCCCGGGGCT	1260
Db	1201	CAGTCCAGCAAGGCTGCAAGCCAGTCCGAGCTCAGCAACAGACCTGCCACCCCGGGGCT	1260
QY	1261	GCAAGTGGGCGCAACGCTGACAGCTGCGAGTGAAGTAACTCAGGCCCTGAGAGGTGATGCT	1320
Db	1261	GCAAGTGGGCGCAACGCTGACAGCTGCGAGTGAAGTAACTCAGGCCCTGAGAGGTGATGCT	1320
QY	1321	GCTGTGCTGCDAAGAGTATATGTGGCCCCCGCAGACCGTATGTCCACCCACGCCACA	1380
Db	1321	GCTGTGCTGCDAAGAGTATATGTGGCCCCCGCAGACCGTATGTCCACCCACGCCACA	1380

QY	1381	GATGAGAAAGTGCACACCCCAAGCCATGATGACAGTGTCAACCCCAAGCACCAGATGGAAGATC	1440
Db	1381	GATGGAAGATGCCACCCCAAGCCCATATATGCAAGTGTCAACCCCAAGCACCAGATGGAAGATC	1440
QY	1441	ACTCCAGCCCACTGATGGAGAGTGCACCCCAAGTCACTGACAGAGAGCGTAACTCCAGCCACT	1500
Db	1441	ACTCCAGCCCACTGATGGAGAGTGCACCCCAAGTCACTGACAGAGAGCGTAACTCCAGCCACT	1500
QY	1501	GATGGAGAGGCCACACAGCCCAACAGAAAGACACTGTGTCCCAACCCCAAGCAGTGTCC	1560
Db	1501	GATGGAGAGGCCACACAGCCCAACAGAAAGACACTGTGTCCCAACCCCAAGCAGTGTCC	1560
QY	1561	ATGTGTGGCCACCAAGCCCACTGTCAACCCCTGATGCGGTATGTGCGCCAGCCGAGACACA	1620
Db	1561	ATGTGTGGCCACCAAGCCCACTGTCAACCCCTGATGCGGTATGTGCGCCAGCCGAGACACA	1620
QY	1621	GCCCCAGAGGGCGCCACAGGCCAGGCTCAACCCCTTAATAAGGGGAAAGAGTGTCTGT	1680
Db	1621	GCCCCAGAGGGCGCCACAGGCCAGGCTCAACCCCTTAATAAGGGGAAAGAGTGTCTGT	1680
QY	1681	TATGCCCAAGAGATCTCAAAAGGAGAGGCAAGCTGATGAGGCAAGCTGTGTAGGGGGGGC	1740
Db	1681	TATGCCCAAGAGATCTCAAAAGGAGAGGCAAGCTGATGAGGCAAGCTGTGTAGGGGGGGC	1740
QY	1741	AGGGGATGTGGCAGAGAGGGTGGGAGATGATGAGGGGCTTCTCACTGTACATTAAGTCAAC	1800
Db	1741	AGGGGATGTGGCAGAGAGGGTGGGAGATGATGAGGGGCTTCTCACTGTACATTAAGTCAAC	1800
QY	1801	TGGATGATATGCCCTGGCTGCCCAATGCCCCCAATCCCAAGTGGGGCAATTAAGGGGTCA	1860
Db	1801	TGGATGATATGCCCTGGCTGCCCAATGCCCCCAATCCCAAGTGGGGCAATTAAGGGGTCA	1860
QY	1861	CGGGAGAGCAGTCCGTCTCTGTGTGTATGTGTGATGTGATGTGGGCGAGCCAGTGGCAG	1920
Db	1861	CGGGAGAGCAGTCCGTCTCTGTGTGTATGTGTGATGTGATGTGGGCGAGCCAGTGGCAG	1920
QY	1921	GCGCGGCCCCAGGCCCTGTGATGATGATCTTGTGTGTCTGTCTTTTGTACTTCACTCAAC	1980
Db	1921	GCGCGGCCCCAGGCCCTGTGATGATGATCTTGTGTGTGTCTTTTGTACTTCACTCAAC	1980
QY	1981	AGTTTCGTTCCTGTGGAGATGTGTGTCTGATGAGGAATCAAGGGGGCTCTGTCTCCCTTC	2040
Db	1981	AGTTTCGTTCCTGTGGAGATGTGTGTCTGATGAGGAATCAAGGGGGCTCTGTCTCCCTTC	2040
QY	2041	CCCTTCCCTTCTTGCTCTCAACATTCGCCCAAGSAGGCGCTGTGAGGTCTCCACACTTCCCA	2100
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QY	2101	GCGCCTAAACTGTGGGCGGCTTGTCCCTGTAGAGCTGTCTCTCCAGCGAGGCCCTGTCAAG	2160
Db	2101	GCGCCTAAACTGTGGGCGGCTTGTCCCTGTAGAGCTGTCTCTCCAGCGAGGCCCTGTCAAG	2160
QY	2161	GTCTTAGGCTCTTGACATGAAAGTGTGTGCTGTGTGTGTGTGGGCGTCTTAAGAGAG	2220
Db	2161	GTCTTAGGCTCTTGACATGAAAGTGTGTGCTGTGTGTGTGTGGGCGTCTTAAGAGAG	2220
QY	2221	ATACAGGCTGTATPAGAGATGACAAAGATGAGGCGAGATGTTTAACTCAGACTTGGC	2280
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QY	2281	ACATGGCTAGAGATCTGTCTCACTAGCTGTGAGGCTCTCAGAGACTGAGAGAAATGAGTA	2340
Db	2281	ACATGGCTAGAGATCTGTCTCACTAGCTGTGAGGCTCTCAGAGAGTGAAGAAATGAGTA	2340
QY	2341	GGAGGGGAGAGCTTCAATTTTGTCTTCTTAAGACCTGTATTTGTGTATTCTCTG	2400
Db	2341	GGAGGGGAGAGCTTCAATTTTGTCTTCTTAAGACCTGTATTTGTGTATTCTCTG	2400
QY	2401	CGTTTCGAGATCTGTGAGAGGGGTGCGCTGTACCTGTAACTCATGAGCTCTTAAGGGA	2460
Db	2401	CGTTTCGAGATCTGTGAGAGGGGTGCGCTGTGTACCTGTAACTCATGAGCTCTTAAGGGA	2460
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QY 2581 TGCTCTTCTAGATGCCCACTCTTACAACTCAATCTCAGCCCAAGAGTCTCTCACTTACG 2640
Db 2581 TGCTCTTCTAGATGCCCACTCTTACAACTCAATCTCAGCCCAAGAGTCTCTCACTTACG 2640
QY 2641 GGCTTCTGATGSCAAATTAATCTGATTTGAGGTTTGGCCCTTTACAGGGGAG 2700
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QY 2701 ATTTTCTGCTCAGTTCAACATGAAATGAGAGAACTCCCTCTTTTACAGCTCACTTC 2760
Db 2701 ATTTTCTGCTCAGTTCAACATGAAATGAGAGAACTCCCTCTTTTACAGCTCACTTC 2760
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QY 2821 GGGTTAAACTCCCAAGTTTCTTGAAGAGGCTCTTGAAGAGTCCCTTTGTCAGACCTTA 2880
Db 2821 GGGTTAAACTCCCAAGTTTCTTGAAGAGGCTCTTGAAGAGTCCCTTTGTCAGACCTTA 2880
QY 2881 CCAAGAGCTGGAATGAGGAGCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db 2881 CCAAGAGCTGGAATGAGGAGCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
QY 2941 CTGGCTTTCTTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db 2941 CTGGCTTTCTTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
QY 3001 TGCTGCTACTGTAACCTGCAATTAATCAATCACTGCAAGCAAGCAAGCAAGCAAGCA 3060
Db 3001 TGCTGCTACTGTAACCTGCAATTAATCAATCACTGCAAGCAAGCAAGCAAGCAAGCA 3060
QY 3061 AAA 3120
Db 3061 AAA 3120
QY 3121 AAAA 3124
Db 3121 AAAA 3124

RESULT 2

US-10-153-921-1
; Sequence 1, Application US/10153921
; Patent No. 6653116
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO0612DIV
; CURRENT APPLICATION NUMBER: US/10153,921
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/207,281
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/734,030
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3124
; TYPE: DNA
; ORGANISM: HOMO SAPIEN
US-10-153-921-1

Query Match 100.0%; Score 3124; DB 4; Length 3124;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCCCCGGCGGGGAGGAAATCCGGTGCCTGGCAAGCGGCTGGCAATGTGGAGGTT 60
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QY 181 CCAACCGGCGCTGCAAGTGAAGCTGGCAATGCCGTTGGGTGTGTGATCTTGGGCGAC 240
Db 181 CCAACCGGCGCTGCAAGTGAAGCTGGCAATGCCGTTGGGTGTGTGATCTTGGGCGAC 240
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QY 541 ATCTGGAACAGGCTACTACTCGAGCGAGACCAAGAGCAAGTGTGTGTGTGTGTGTGT 600
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Db 661 CTGGTTTACTAACAACGCTGAGAACTGAGATTTGATAGTGAATCTTCACTGAGCT 720
QY 721 AAGCTGAAGATGAGCTCATCAAGAGCCCTGTGGGACCCCGAGTATCTGAGCCCAAG 780
Db 721 AAGCTGAAGATGAGCTCATCAAGAGCCCTGTGGGACCCCGAGTATCTGAGCCCAAG 780
QY 781 GTGTGAGCGGAGAGGATGAGAGCCCTGTGAGCTGTGAGGAGGAGGAGGAGGAGGAG 840
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QY 841 TACATCTGCTTTCAGGCAATCACTTCTATGAGAGGAGGAGGAGGAGGAGGAGGAG 900
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QY 901 AACCATGATGAAGATCTTTCGCAAGATCCGCGGAGGAGGAGGAGGAGGAGGAGGAG 960
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QY 961 TATTGGATGATATTTCGAGGAGCAAGAGCTGTGTCAAGAGCTGTGTGTGTGTGTGT 1020
Db 961 TATTGGATGATATTTCGAGGAGCAAGAGCTGTGTCAAGAGCTGTGTGTGTGTGTGT 1020
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Db 1021 CAAGACCAGGGATCACTGAGAGAGAGGACCTCTCCATGAGTGAATTTCTGGCAATGCT 1080
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Db 1081 GCTTCTGATTAAGAACTCAAGAGATGCTGTGTGCTGCCAGATTGAAAAAGAACTTTGCCAGG 1140
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QY 2461 AGGAGGAACAATTAGACGATGAGAGCCTGGACAGGAGAGTAAACAAGCCAGAC 2520
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Db 2641 GGGTGTGATGAGCAATTAATCTGATTAATGAGAGTGGTGGCTTTACAGGGGAG 2700
QY 2701 ATTTTGTGCTCAGTCAACAATGAATGAAGAGAACTCCCTCTTCTCAAGCTCACTTC 2760
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Db 2821 GGGTTAACTCCCAAGTTTCTGAGGGAGGCTCTGAAGAGTCCCTTTGTCTAGACCTTA 2880
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QY 3061 AA 3120
Db 3061 AA 3120
QY 3121 AAAA 3124
Db 3121 AAAA 3124

Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dimaac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ. ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ. ID NO 20
LENGTH: 2840
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (206)..(1711)
US-09-620-312D-20
Query Match 89.3%; Score 2791.2; DB 4; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

465 ATGTGTTTGTGACCCCGAAGAGTAATTCTTCTCTGAGACTGCCACGGGAGGAGG 524
530 TGTTTGACTGGAATCTGTGACCAAGGACTACTCTGAGACGAGACACAAGCAACGTGTAC 589
525 TGTTTGACTGGAATCTGTGACCAAGGACTACTCTGAGACGAGACACAAGCAACGTGTAC 584
590 GGCAGTCTCTGAGGCGGTGCTTATTTGGACTCACTCAAGATGTGTGACAGGAATCTCA 649
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830 GAGTATCATGTATCATCTGCTTTCAAGCATCCACTTTTATGAGAGGTGAAAG 889
825 GAGTATCATGTATCATCTGCTTTCAAGCATCCACTTTTATGAGAGGTGAAAG 884
890 ATGATTATGAGAACCATGATAGAAATCTCTCCGAGATCTGTGATGATGAT 949
885 ATGATTATGAGAACCATGATAGAAATCTCTCCGAGATCTGTGATGATGAT 944
950 TTGACTTCCATATTGGAGTATATTTCGAGGAGCCAAAGACTGTGCAAAAGCTGA 1009
945 TTGACTTCCATATTGGAGTATATTTCGAGGAGCCAAAGACTGTGCAAAAGCTGA 1004
1010 TGGAGTGTAGACAGACCAAGGATCACTGTGAGAAAGGCAATCTCCATATGTGATTT 1069
1005 TGGAGTGTAGACAGACCAAGGATCACTGTGAGAAAGGCAATCTCCATATGTGATTT 1064
1070 CTGGCAATGCTGCTTCTGTATTAAGAAATCAAGATGTGTCTGTGCCAATTAAGAA 1129
1065 CTGGCAATGCTGCTTCTGTATTAAGAAATCAAGATGTGTCTGTGCCAATTAAGAA 1124
1130 ACTTGGCCAGGCGCAAGTGAAGAAAGCTGTCCAGTGAACCACTCATGAAACGCTCC 1189
1125 ACTTGGCCAGGCGCAAGTGAAGAAAGCTGTCCAGTGAACCACTCATGAAACGCTCC 1184
1190 GGGCAACAGAGAGTCCAGCAAGGCTGACGCCAGTGGGCTTCAGCCACAGACACTGCA 1249
1185 GGGCAACAGAGAGTCCAGCAAGGCTGACGCCAGTGGGCTTCAGCCACAGACACTGCA 1244
1250 CCCCCGGGCTGTGAGGTGGGCTCACAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1309
1245 CCCCCGGGCTGTGAGGTGGGCTCACAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1304
1310 AGGGTATGCTGCTGTGCTGCAAAAGAGTGAATATGTGGCCCCCGAGACCGTGTGCA 1369
1305 AGGGTATGCTGCTGTGCTGCAAAAGAGTGAATATGTGGCCCCCGAGACCGTGTGCA 1364
1370 CCCCAGCCACAGATGGAAGTGCACCCAGCCACTGATGAGAGTGTCAACCCAGCCACCG 1429
1365 CCCCAGCCACAGATGGAAGTGCACCCAGCCACTGATGAGAGTGTCAACCCAGCCACCG 1424
1430 ATGGAAGCATCATCTCAGCCACTGATGGAAGTGTCAACCCAGCATCTGACAGAGCGCTA 1489
1425 ATGGAAGCATCATCTCAGCCACTGATGGAAGTGTCAACCCAGCATCTGACAGAGCGCTA 1484
1490 CTCGAGCCACTGATGGAAGAGCCACACAGCCACAGAAAGACACTGTGCCACCAACCC 1549
1485 CTCGAGCCACTGATGGAAGAGCCACACAGCCACAGAAAGACACTGTGCCACCAACCC 1544
1550 AAAGAGTGCATGCTGTGCAACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1609
1545 AAAGAGTGCATGCTGTGCAACAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAG 1604

QY 1610 CGGACGACACAGCCCCAGAGGGGCGCACAGGCGAGGCTCCACCCCTCTAGTAAAGGGAGG 1669
DB 1605 CGGACGACACAGCCCCAGAGGGGCGCACAGGCGAGGCTCCACCCCTCTAGTAAAGGGAGG 1664
QY 1670 AGGCTGCTGCTTATGCTCCCGAGAGTCTCAAAAGGAGAGGCGGAGCTGATAGGCAAGCTTGG 1729
DB 1665 AGGCTGCTGCTTATGCTCCCGAGAGTCTCAAAAGGAGAGGCGGAGCTGATAGGCAAGCTTGG 1724
QY 1730 TAGAGGGGGGCGAGGGGATGGGAGAGGGGTGGGAGAGTGAAGAGGGCTTCTCACTGTA 1789
DB 1725 TAGAGGGGGGCGAGGGGATGGGAGAGGGGTGGGAGAGTGAAGAGGGCTTCTCACTGTA 1784
QY 1790 CATAGAGTCACTGGACATGATGCTCCCTCCCATGCCCCACATCCCACTGAGGGGAGTA 1849
DB 1785 CATAGAGTCACTGGACATGATGCTCCCTCCCATGCCCCACATCCCACTGAGGGGAGTA 1844
QY 1850 ACTAGGGGGTCAAGGGAGAGACATCTGCTCTGCTGATATGTGTGATGATGGGGAG 1909
DB 1845 ACTAGGGGGTCAAGGGAGAGACATCTGCTCTGCTGATATGTGTGATGATGGGGAG 1904
QY 1910 GCGAGTGGAGGGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1969
DB 1905 GCGAGTGGAGGGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1964
QY 1970 CTAGCTTCAACAGATTCTGCTCTGCTGAGATGCTGCTGATAGGATCTCAAGGGGCTCC 2029
DB 1965 CTAGCTTCAACAGATTCTGCTCTGCTGAGATGCTGCTGATAGGATCTCAAGGGGCTCC 2024
QY 2030 TGTCTCTCTTCCCTTCCCTTCTGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTG 2089
DB 2025 TGTCTCTCTTCCCTTCCCTTCTGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTG 2084
QY 2090 AACACTCTCCCAAGGCGCTTAACTTGGGCGGCGCTTGGCTGAGAGCTGCTGCTGAGGAG 2149
DB 2085 AACACTCTCCCAAGGCGCTTAACTTGGGCGGCGCTTGGCTGAGAGCTGCTGCTGAGGAG 2144
QY 2150 CCCTGTCAGGGGCTTAGGCTCCTGACATGAAAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 2209
DB 2145 CCCTGTCAGGGGCTTAGGCTCCTGACATGAAAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 2204
QY 2210 TCTAGAGAGAGATACAGGCTGATATAGAGATGACAGAAAGTGAAGGCAATGTTTAAAT 2269
DB 2205 TCTAGAGAGAGATACAGGCTGATATAGAGATGACAGAAAGTGAAGGCAATGTTTAAAT 2264
QY 2270 CCGAGCTTGGACATGAGGATGAGGATATCTGCTCACTGCTGAGAGTCTCTCAAGAGTGA 2329
DB 2265 CCGAGCTTGGACATGAGGATGAGGATATCTGCTCACTGCTGAGAGTCTCTCAAGAGTGA 2324
QY 2330 GAGAAATGAGTGAAGAGGGGACAGAACTTCCATTTTGTCTTCTTCTTCTTCTTCTTCTT 2389
DB 2325 GAGAAATGAGTGAAGAGGGGACAGAACTTCCATTTTGTCTTCTTCTTCTTCTTCTTCTT 2384
QY 2390 GTTATTTCTGCTTCCGAGTCTCTGAGTGGGCTCCCTGTAACCTGTAACCTGTAACCTG 2449
DB 2385 GTTATTTCTGCTTCCGAGTCTCTGAGTGGGCTCCCTGTAACCTGTAACCTGTAACCTG 2444
QY 2450 CTCTAAGGAGAGAGAGAGCAATTAGAGCGTGGCAATGAGACCTGGCAGGGGAGATACA 2509
DB 2445 CTCTAAGGAGAGAGAGAGCAATTAGAGCGTGGCAATGAGACCTGGCAGGGGAGATACA 2504
QY 2510 AGCCCGAGACCCAGTGTCCAGCTTACTGAGTCTTAACTTGGGAGGAGGAGGAGGAGG 2569
DB 2505 AGCCCGAGACCCAGTGTCCAGCTTACTGAGTCTTAACTTGGGAGGAGGAGGAGGAGG 2564
QY 2570 TGAATCCTCTTGTCTTCTTCTAGATGCCACTCTTCAATCTCAAGCCCAAGATCTCT 2629
DB 2565 TGAATCCTCTTGTCTTCTTCTAGATGCCACTCTTCAATCTCAAGCCCAAGATCTCT 2624
QY 2630 CCAACCTTGAAGGGGCTTGTCTCATGAGCAATTAATCATATCTGAATTTGAGGTTTGGCTT 2689
DB 2625 CCAACCTTGAAGGGGCTTGTCTCATGAGCAATTAATCATATCTGAATTTGAGGTTTGGCTT 2684

QY 2690 TACAGGGGAGAGATTTTCTGCTGATCTCAACATGAAGAGAGAACTCCCTTTCTA 2749
DB 2685 TACAGGGGAGAGATTTTCTGCTGATCTCAACATGAAGAGAGAACTCCCTTTCTA 2744
QY 2750 CAGCTCACTCTTATCAAGAGGCGGAGGCTGCTGAGAGCCACATTTGATTTTCTGGG 2809
DB 2745 CAGCTCACTCTTATCAAGAGGCGGAGGCTGCTGAGAGCCACATTTGATTTTCTGGG 2804
QY 2810 ATGAGAGATGAGGTTAACTCCCGAGTTTCTGAG 2845
DB 2805 ATGAGAGATGAGGTTAACTCCCGAGTTTCTGAG 2840

RESULT 4
US-09-620-312D-19
Sequence 19, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundang
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 19
LENGTH: 2747
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (206) .. (1618)
US-09-620-312D-19

Query Match 83.1%; Score 2595.2; DB 4; Length 2747;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2700; Conservative 0; Mismatches 3; Indels 93; Gaps 1;

QY 50 TGCTGAGAGTTCGTAGCCGAGAGGCGTGTGATGCGCGGCTTGGCCCCGGGTGCTG 109
DB 45 TGCTGAGAGTTCGTAGCCGAGAGGCGTGTGATGCGCGGCTTGGCCCCGGGTGCTG 104
QY 110 GAGCGGATTCGCGCGCGCTTCCGAGAGCCCTGGCGCCCCCGCTGAGCCCGATCACTT 169
DB 105 GAGCGGATTCGCGCGCGCTTCCGAGAGCCCTGGCGCCCCCGCTGAGCCCGATCACTT 164
QY 170 CCTCCCTGTAGCAACCGGCGGCTGAGGTTAGAGCTTGGCAAGCCGTTGGGATGTGA 229
DB 165 CCTCCCTGTAGCAACCGGCGGCTGAGGTTAGAGCTTGGCAAGCCGTTGGGATGTGA 224
QY 220 CTCGGGCGGAGAGAGAGATTAATCAGGCAATGAGAGTGAAGATATGATTTGG 289

Db 225 CTCTGGCGGCAAGAAAGTATTAACCAAGCATCGAGGTGAATGATATTGG 284
 QY 290 GACAGGTCAATCAAGACTGAGGAGTTTGTGAATCTTCCGGGCAAGACAAGACAG 349
 Db 285 GACAGGTCAATCAAGACTGAGGAGTTTGTGAATCTTCCGGGCAAGACAAGACAG 344
 QY 350 GCAAGGTGCAACCTCGCAAGAGTTCCAGAGCGGACCGCAAGGTGCGGAAAGCTG 409
 Db 345 GCAAGGTGCAACCTCGCAAGAGTTCCAGAGCGGACCGCAAGGTGCGGAAAGCTG 404
 QY 410 CCAAGAACGAGATAGGATCTTCAAGATGATGAAGATCCCAATCTTCAAGCTGTG 469
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 Db 465 ATGTGTTTGAACCCGCAAGAGTATCTTATCTTCTGAGCTGGGCAAGGGAGAG 524
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 Db 525 TGTGTCCTGATCTGACCAAGGCTACTCTCGAGCGAGACAAGAGCAAGTGTAC 584
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 Db 585 GCAAGGTCTGAGAGCGCGTGTATTTGCACTCACTCAAGATCTGCAAGAGATCTCA 644
 QY 650 AGCTGAGAACCTGTGTTTACTCAACCGGCTGAAGAACTGGAAGATTGTCACTAGT 709
 Db 645 AGCTGAGAACCTGTGTTTACTCAACCGGCTGAAGAACTGGAAGATTGTCACTAGT 704
 QY 710 TCCATCTGGTAAAGTAAAGATGCGCTCAACAAGAGCCGTGGGACCCCGGATAC 769
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 Db 765 TGGCCCAAGAGTGTAGCGCGGCAAGGATGAAGAGCCCTGTGTGAGCTGTGGACATTG 824
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 Db 825 GAGTCATCATGTACATCTGCTTTCAGGCAATCACCTTCTTAAGAAGTGAAGAG 884
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 Db 885 ATGATTATGAAGCAATGATTAAGATCTCTTCCGCAAGATCTGTGCTGTGATGAGT 944
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 Db 945 TTGATCTTCAATTTGGGATGATATTTCCGAGGCAAGCAAGCTGTGTCAAGAGCTTA 1004
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 Db 1005 TGGAGGTGAGCAAGACCAAGGATCACTGCAAGAGGCAATCTCCATGATGATTT 1064
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 Db 1065 CTGCAATGCTGCTTCTGATTAAGAACATCAAGAGTGTGTCTGTGCCAAGATTGAAGA 1124
 QY 1130 ACTTTGCAAGGCGCAAGTGAAGAGGCTGTCCGAGTGACCAACCTCTCATGAACGCGCTCC 1189
 Db 1125 ACTTTGCAAGGCGCAAGTGAAGAGGCTGTCCGAGTGACCAACCTCTCATGAACGCGCTCC 1184
 QY 1190 GGGGACCAAGAGAGTCCAGAGCGGCTGCAAGCGGCTGAGGCAAGACATGCGCA 1249
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 Db 1245 CCCCCGGGCT----- 1255
 QY 1310 AGGTGATGCTGCTCTGCTGCAAGAGTATATGTTGGCCCCCGCAAGCTGATGCGCA 1369
 Db 1256 -----GCAGACCTGATGCGCA 1271

QY 1370 CCCCAGCCACAGATGGAAGTGCACCCCAAGCACTGATGCGAGTGTCAACCCCAAGCCAG 1429
 Db 1272 CCCCAGCCACAGATGGAAGTGCACCCCAAGCACTGATGCGAGTGTCAACCCCAAGCCAG 1331
 QY 1430 ATGGAAGCATCTCCAGCCACTGATGGAAGTGTCAACCCCAAGCACTGACAGAGCCCTTA 1489
 Db 1332 ATGGAAGCATCTCCAGCCACTGATGGAAGTGTCAACCCCAAGCACTGACAGAGCCCTTA 1391
 QY 1490 CTCCAGCCACTGATGGAAGTGCACCCCAAGCACTGATGCGAGTGTCAACCCCAAGCC 1549
 Db 1392 CTCCAGCCACTGATGGAAGTGCACCCCAAGCACTGATGCGAGTGTCAACCCCAAGCC 1451
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 Db 1452 AAAGAGTGCATGCTGGGCAACCAAGGAGTGTCAACCCCAAGCCAGCTATGAGCCAGC 1511
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 Db 1512 CGGACAGCACAGCCCAAGAGGCGCCACAGGCTAGGCTCCACCTCTAATAAGGGAGAG 1571
 QY 1670 AGGCTGCTGTTATGCCAGAGTCTCAAGAGGAGAGGCAAGCTGATGAGGAGCTG 1729
 Db 1572 AGGCTGCTGTTATGCCAGAGTCTCAAGAGGAGAGGCAAGCTGATGAGGAGCTG 1631
 QY 1730 TGAAGGGGGGCAAGGAGTGGGCAAGAGGAGTGGAGTGAAGAGGAGCTTCTCACTGTA 1789
 Db 1632 TGAAGGGGGGCAAGGAGTGGGCAAGAGGAGTGGAGTGAAGAGGAGCTTCTCACTGTA 1691
 QY 1790 CATAGAGTCACTGGAGATGATGCTGCTCCCGCATGCGCCCAATCCAGTGGGGCATTA 1849
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 QY 1850 ACTAGGGGTCAAGGAGAGCAAGTCTGCTCTCTGTGTATGTGTGATGTGAGTGTGGAG 1909
 Db 1752 ACTAGGGGTCAAGGAGAGCAAGTCTGCTCTCTGTGTATGTGTGATGTGAGTGTGGAG 1811
 QY 1910 GCGAGTGGCAAGGCGCGCCCAAGGCGCCCGCATGAGATCTTGTGGCTTTTCTGTCTTTG 1969
 Db 1812 GCGAGTGGCAAGGCGCGCCCAAGGCGCCCGCATGAGATCTTGTGGCTTTTCTGTCTTTG 1871
 QY 1970 CTAGCTTACCAAGTTTCTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2029
 Db 1872 CTAGCTTACCAAGTTTCTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1931
 QY 2030 TGCCTCTCTCCCTCCCT 2089
 Db 1932 TGCCTCTCTCCCTCCCT 1991
 QY 2090 AACCTCTCCAGGCGCTTAACTTGGGCGGCGCTTCCCTGAGAGCTGTCTCTCAAGCGAG 2149
 Db 1992 AACCTCTCCAGGCGCTTAACTTGGGCGGCGCTTCCCTGAGAGCTGTCTCTCAAGCGAG 2051
 QY 2150 CCTGTGACGCGTCTTGAAGCTCTCTGACATGAAGTGTGTGTGTGTGTGTGTGTGTGTGT 2209
 Db 2052 CCTGTGACGCGTCTTGAAGCTCTCTGACATGAAGTGTGTGTGTGTGTGTGTGTGTGTGT 2111
 QY 2210 TCTAGGACAGATCAGGCTGTATGAAGGATGAAGAGTGAAGGAGTGAAGTGTGTAGT 2269
 Db 2112 TCTAGGACAGATCAGGCTGTATGAAGGATGAAGAGTGAAGGAGTGAAGTGTGTAGT 2171
 QY 2270 CCAGACTTGGACATAGGCTAGGATATCTGCTCACTAGCTGTGAGAGTCTTCAAGAGTGA 2329
 Db 2172 CCAGACTTGGACATAGGCTAGGATATCTGCTCACTAGCTGTGAGAGTCTTCAAGAGTGA 2231
 QY 2330 GAGAAATGAGTGAAGAGGAGGAGAGCTTCCATTTTGTCTTCTTAAGACCTGTATTGT 2389
 Db 2232 GAGAAATGAGTGAAGAGGAGGAGAGCTTCCATTTTGTCTTCTTAAGACCTGTATTGT 2291
 QY 2390 GTTATTTCTGCTCTTCCGAGTCTGTCAGTGTGGGCTGCGCTGTACCTGAACTCATAGGC 2449
 Db 2292 GTTATTTCTGCTCTTCCGAGTCTGTCAGTGTGGGCTGCGCTGTACCTGAACTCATAGGC 2351

Db 5239 TCCTGACATGAGGCTGCTGCTGATACCTGATACCTGATGAGCTCTTAAGGAAAGAGAAACA 5298
QY 2471 ATTAGAGAGTGGCAATGAGACCTGGCAGAGGAGATACAGCCAGCAAGAGTGTCCCA 2530
Db 5299 ATTAGAGAGTGGCAATGAGACCTGGCAGAGGAGATACAGCCAGCAAGAGTGTCCCA 5358
QY 2511 GCGTTACTGGGCTCTTACCTGGGCAAGAGGAGGCTATACCTCTTCTCTTCT 2590
Db 5359 GCGTTAATGGGCTCTTACCTGGGCAAGAGGAGGCTATACCTCTTCTCTTCT 5418
QY 2591 AGATGCCACCTCTCTCAATCATCTGACCCAGTCTCTTCCACCTTAGGGGCTTGTGCTG 2650
Db 5419 AGATGCCACCTCTCTCAATCATCTGACCCAGTCTCTTCCACCTTAGGGGCTTGTGCTG 5477
QY 2651 ATGGCAATACCTCATATCTGATTTGAGGTTTGGCCCTTTACAGGGGAGATTTTCTGCT 2710
Db 5478 ATGGCAATACCTCATATCTGATTTGAGGTTTGGCCCTTTACAGGGGAGATTTTCTGCT 5537
QY 2711 CAGTTCAACATGAAATGAAGAGAACTCCCTCTTTCTACAGCTCACTTCTATCAGAGGC 2770
Db 5538 CAGTTCAACATGAAATGAAGAGAACTCCCTCTTTCTACAGCTCACTTCTATCAGAGGC 5597
QY 2771 CCAGTGCTCAGAGCCCATTTGATGCTTTTCTGGGATGAGGAGTAACT 2830
Db 5598 CCAGTGCTCAGAGCCCATTTGATGCTTTTCTGGGATGAGGAGTAACT 5657
QY 2831 CCCAGTTCTCTGAGGAGGCTCTCTGACAGGCTGCTTGTGACAGCTCAACAGGCTG 2890
Db 5658 CCCAGTTCTCTGAGGAGGCTCTCTGACAGGCTGCTTGTGACAGCTCAACAGGCTG 5717
QY 2891 GATAGGAGCCACATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2950
Db 5718 GATAGGAGCCACATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5777
QY 2951 CCCGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3010
Db 5778 CCCGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5837
QY 3011 CTGAACCTGGCAATTAACATCACTCCCTGCAAGGC 3045
Db 5838 CTGAACCTGGCAATTAACATCACTCCCTGCAAGGC 5872

RESULT 6
US-10-153-921-3
Sequence 3, Application US/10153921
Patent No. 6653116
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLO00612DIV
CURRENT FILING DATE: US/10/153,921
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/207,281
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/734,030
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 7542
TYPE: DNA
ORGANISM: HOMO SAPIEN
US-10-153-921-3

Query Match 60.1%; Score 1876.6; DB 4; Length 7542;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1151 AGAAGGCTGTCGAGTGAACCACTCATGAACGGCTCCGGGACCAAGAGAGTCCAGCA 1210
|||||

Db 3979 AGAAGGCTGTCGAGTGAACCACTCATGAACGGCTCCGGGACCAAGAGAGTCCAGCA 4038
QY 1211 CGGCTCAGGCCAGTGGGCTTACGACCAAGACTGCAACCCCGGGGCTGAGGTGGG 1270
Db 4039 CGGCTCAGGCCAGTGGGCTTACGACCAAGACTGCAACCCCGGGGCTGAGGTGGG 4098
QY 1271 CCAAGCTGAGTGGGAGTGAAGTCACTCAGCCCTGAGGGGTGATGCTGCTGCTG 1330
Db 4099 CCAAGCTGAGTGGGAGTGAAGTCACTCAGCCCTGAGGGGTGATGCTGCTGCTGCTG 4158
QY 1331 CAAAGGTATATATGTTGGCCCCCGGACGATAGTCCCAACCCAGCAAGATGAAAGT 1390
Db 4159 CAAAGGTATATATGTTGGCCCCCGGACGATAGTCCCAACCCAGCAAGATGAAAGT 4218
QY 1391 CCAACCCAGCACTGATGAGTGAACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1450
Db 4219 CCAACCCAGCACTGATGAGTGAACCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 4278
QY 1451 CTGATGAGAGTGTCAACCCAGTCACTGACAGAGGCTACTCAGGCACTGATGAGAG 1510
Db 4279 CTGATGAGAGTGTCAACCCAGTCACTGACAGAGGCTACTCAGGCACTGATGAGAG 4338
QY 1511 CCAACACAGCCACAGAGAGAGACTGTGCTCCACCAACCAAGCAAGTGCATGCTG 1570
Db 4339 CCAACACAGCCACAGAGAGAGACTGTGCTCCACCAACCAAGCAAGTGCATGCTG 4398
QY 1571 CCAAGGCACTGCAACCCCTGAGCCGGGCTATGAGCCAGCCAGCCAGCCAGCCAGCC 1630
Db 4399 CCAAGGCACTGCAACCCCTGAGCCGGGCTATGAGCCAGCCAGCCAGCCAGCCAGCC 4458
QY 1631 GCGCCACAGGCAAGGCTCAACCTCTAGTAAAGGGAAGAGGCTCTGTTATGCCCCAG 1690
Db 4459 GCGCCACAGGCAAGGCTCAACCTCTAGTAAAGGGAAGAGGCTCTGTTATGCCCCAG 4518
QY 1691 AGTCTCAAGGAGAGAGGCACTGATGAGGAGCTGTGTAAGGAGGAGGAGGAGTGG 1750
Db 4519 AGTCTCAAGGAGAGAGGCACTGATGAGGAGCTGTGTAAGGAGGAGGAGGAGTGG 4578
QY 1751 CAGAGAGGTGGAGAGTGAATAGAGGAGCTTCACTGATCAATAGTCACTGATGAT 1810
Db 4579 CAGAGAGGTGGAGAGTGAATAGAGGAGCTTCACTGATCAATAGTCACTGATGAT 4638
QY 1811 CCCTGCTCCCAATGCCCCCAATCCAGTGGGATTAATAGAGGATCAAGGAGAGCA 1870
Db 4639 CCCTGCTCCCAATGCCCCCAATCCAGTGGGATTAATAGAGGATCAAGGAGAGCA 4698
QY 1871 GTCTGCTCTCTGT 1930
Db 4699 GTCTGCTCTCTGT 4758
QY 1931 AGCCCCGATGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1990
Db 4759 AGCCCCGATGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4818
QY 1991 CTTTGTGGATGCTGCTAGAGGATCTCAGAGGAGGCTCTGCTCTCTCTCTCTCTCT 2050
Db 4819 CTTTGTGGATGCTGCTAGAGGATCTCAGAGGAGGCTCTGCTCTCTCTCTCTCTCT 4878
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Db 4879 CTTGCTCAACATTCCTTGGGCTTTTCTGCTCTTGTCTAGCTTCAACGATTTCTGT 4938
QY 2111 TTGGGAGGCTTGGCTTGAAGCTGCTCTCAGAGGAGGCTCTCAGAGGCTCTTGAAGCT 2170
Db 4939 TTGGGAGGCTTGGCTTGAAGCTGCTCTCAGAGGAGGCTCTCAGAGGCTCTTGAAGCT 4998
QY 2171 CTTGCAATGAAGT 2230
Db 4999 CTTGCAATGAAGT 5058
QY 2231 GTATAGAGAGTCAAAAGTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2290
Db 5059 GTATAGAGAGTCAAAAGTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5118

QY 2291 GGATACCTGCTCACTAGCTGTGAGGTCTTCAGAGTGTGAGAGAAATGATGAGAGGAGGAGAG 2350
DB 5119 GGATACCTGCTCACTAGCTGTGAGGTCTTCAGAGTGTGAGAGAAATGATGAGAGGAGAGAG 5178
QY 2351 AGCTTCATTTTGTGCTTCTCTAGAGCCCTGTTATTGTTGTTATTTCTGCTTTCCAG 2410
DB 5179 AGCTTCATTTTGTGCTTCTCTAGAGCCCTGTTATTGTTGTTATTTCTGCTTTCCAG 5238
QY 2411 TCCTGAGTGGGTGCTGCTGTGACCTGAACTCATGAGCTCTAAGGAAAGAGAGAGCA 2470
DB 5239 TCCTGAGTGGGTGCTGCTGTGACCTGAACTCATGAGCTCTAAGGAAAGAGAGAGCA 5298
QY 2471 ATTAGACGTGGCAATGAGACCTGGAGGAGCAAGTACAGCCAGACCCAGTGTCCA 2530
DB 5299 ATTAGACGTGGCAATGAGACCTGGAGGAGAGTACAGCCAGACCCAGTGTCCA 5358
QY 2531 GCCTTACGTGGTCTTACCTGTGGCCAAACAGGAGGAGTGTATCTCTCTCTCTCT 2590
DB 5359 GCCTTATGGTCTTACCTGTGGCCAAACAGGAGGAGTGTATCTCTCTCTCTCTCT 5418
QY 2591 AGATGCCACCTGCTCAATCTCAGCCCAAGTCTCTCCACCTAGGAGGAGTGTCTGC 2650
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QY 2651 ATGGCAATACCTCATATCTGATTTGAGGTTTGCCTTTACAGGAGGAGATTTTCTGCT 2710
DB 5478 ATGGCAATACCTCATATCTGATTTGAGGTTTGCCTTTACAGGAGGAGATTTTCTGCT 5537
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DB 5538 CAGTTCACATGAAATGAAAGAACTCCTCTTTCTACAGCTCACTTATCAGAGGC 5597
QY 2771 CCAGGTGCTCAGAGCCACATGAGTCTTTTCTGGAGTGTGAGGAGTGTAACT 2830
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QY 2831 CCCAGTTTCTGAGGAGGAGTCTCAGAGTGTGCTTGTGAGACCCCTACAGAGCCCTG 2890
DB 5658 CCCAGTTTCTGAGGAGGAGTCTCAGAGTGTGCTTGTGAGACCCCTACAGAGCCCTG 5717
QY 2891 GATAGCAGCCACATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2950
DB 5718 GATAGCAGCCACATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5777
QY 2951 CCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3010
DB 5778 CCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5837
QY 3011 CTGAACCTGGCAATTAACATCACCTGTGAAGCC 3045
DB 5838 CTGAACCTGGCAATTAACATCACCTGTGAAGCC 5872

RESULT 7
US-09-205-258-74
Sequence 74, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0

RESULT 9
US-09-016-434-1454
Sequence 1454, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1454:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g790789
US-09-016-434-1454

Query Match 8.5%; Score 265.8; DB 4; Length 1480;
Best local Similarity 54.7%; Pred. No. 7,1e-51;
Matches 611; Conservative 0; Mismatches 471; Indels 35; Gaps 3;

QY 100 CCGGTCCTGGAGAGGATTCCTGCGCGCGCTCCCGGAGCCCTCGGCGCCCGCTGAGCCC 159
DB 30 CCGAGCAGCGAGCGGCGGTGAGGACCGCGCCACAGCTCGGCGCGCAACACCGCGGCGCTC 89

QY 160 GCGATCACTTCCTCCCTGTGACCAACCGGCGCTGACAGGTTAAGAGCTTGCAATGCCGTTT 219
DB 90 CCGAGCAGCGCGCCGNNNGAGCCCGAGANCCCTGGCTGTGTGCGGGGCGCACTGGGCGCAT 149

QY 220 GGGTGTGTGCTGTGGCGCAGAAAGAACTAATACCAAGCATCGAGGCTGACTGACAGA 279
DB 150 GCTGGGGGCGAGTGAAGCGCCCG-----GTGGAACAGCGCGAGCACTTGAAGCATC 204

QY 280 TATGATTTGGAGCAGGTCACTCAAGACTGAGAGATTGTTGAAATCTTCCGGGCGCAAGAC 339
DB 205 TAGGACTTTCGAGATGTCTGGGCGAGGGGCGCTTTCGAGAGTGAATCTTGCGAGAAAT 264

QY 340 AAGAGCAGCGCAGCTGACACCTCCAGAAAGTTCCAGAGCGGAGCGGCGCAAGGTG 399
DB 265 AAGAGAGCGAGAGCTGTGGCGCATCAATGATTCAGAGAGGCGCTGAGGGCAAG 324

QY 400 CCGAAGCTGCCAAGACGAGATAGGATCTCAAGATGTGAGAGATCCCAATCTTA 459
DB 325 GAAGGAGCATGAGAGATAGATTTGCTGTCTGCACAGATCAAGACCCCAATTTGA 384

QY 460 CAGCTGTGATGTGTTTGTGACCCGCAAGAGTACTTATCTTCTGGAGCTGGCGACG 519
DB 385 GCGCTGATGATCATATATAGATGTGGGGCGACCTTACTCTATATAGAGCTGGGTG 444

QY 520 GGAAGGAGGTGTTTGACTGATCTGACACAGGCTACTTCTCGAGGAGACACAGC 579
DB 445 GTGGGAGAGCTTTTGAACCGTATTTGGAAAAAGGCTTCTACACGAGCGGACGCGAC 504

QY 580 AAGTGTACGGAAGTCTGTGAGGCGCGGCTTATTTGACCTCAAGATCGGAC 639
DB 505 CGCTCATCTTCAGGTGTGATGTGTGAATATCTCATGACCTGGGCAITGTAC 564

QY 640 AGGATCTCAAGCTGGAGAACCTGTTTACTACAAACCGGCTGAGAACTGAAATGTG 699
DB 565 CCGGATCTCAAGCCAGAGATCTGCTGTACTACAGCTGAGTGAAGACTCCAAAATCAG 624

QY 700 ATCACTGACTTCATCTGCTAAGCTAAGAAA-----TGCCCTCATCAGAGCCCTGT 753
DB 625 ATCTCGAGCTTGGCTCTCCAGATGAGAGCCGCGCAGTGTGTCTCCACCGGCTGT 684

QY 754 GGAACCCCGAGTATCTGCGCCCGAGGTGTAGGCGGCGAGCGGTATGAGAGCCCTGT 813
DB 685 GGAATCTCGGAGTACGTGGCGCCCTGAAGTCTGGCCCAAGGCTTACAGCAAGGCTGTG 744

QY 814 GAGTGTGGGCGCATTTGAGATCATGTACATCCGCTTTCAGGCAATCACTTCTAT 873
DB 745 GATGTGTGTCTCAATAGGTGTATGCTTCTGCTTCTGCTGCTTCTGCTTCTAT 804

QY 874 GAGAGGTGGAAGAGATGATTATGAAACATGATAGATCTTCCGCAAGATCTG 933
DB 805 GAGGAG-----AATGAGCCAACTCTTTGAACGATTTTG 840

QY 934 GCTGTGACTATAGATTGATCTCTCATATTTGGATGATATTTGCGAGCGCAAGAC 993
DB 841 AAGGCGAGTACAGATTTGATCTCTCTTACTGGAGCAGATCTGATCTTGGCAAGAT 900

QY 994 CTGTCAAGGCTGATGAGGTGAGAGCAAGACCAAGGATCTCTCAAGAGGCGCATC 1053
DB 901 TTATTCGGGCACTGTATGAGAGGACCCAGAAAAAGTTCCTGTGAGCGGCTTG 960

QY 1054 TCCATAGTGAATTTCTGCAATGCTGCTTGTATAGAACTCAAGATGTGTCTGT 1113
DB 961 CAGCAGCCATGATTTGAGAGATACAGCTTATGATTAAGATTTCCACAGTGGTGAAT 1020

QY 1114 GCCCAGATTGAAAAAGATTTCAGAGGCGCAAGTGAAGAGGCTGTCCGATGACACC 1173
DB 1021 GAGAGATTCAGAAAGAACTTTGCCAAGAGCAAGTGAAGAACCTTCAATGCGAGGCT 1080

QY 1174 CTATGAAGCGCTCCGCGCACCAGAGCACTCCAGCA 1210
DB 1081 GTGTTGCGGCAATGAGGAATCTGACGTGGGACCA 1117

RESULT 10
US-09-016-434-543
Sequence 543, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA

Thu Apr 29 08:44:17 2004

us-10-669-689-1.rn1

Page 13

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COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTTUT02
CLONE: 2342912
US-09-016-434-543
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Query Match 8.3%; Score 258; DB 4; Length 264;

Best Local Similarity 97.7%; Pred. No. 1,9e-49;

Matches 258; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 515 CCACGGGAGGAGGAGTGTTCATCTGATCGATCGACACAGGCTACTACTCGAGAGGAGACA 574
DB 1 CCACNGAGAGGAGAGTGTTCATCTGATCGATCGACACAGGCTACTACTCGAGAGGAGACA 60
QY 575 CAACGAACTGTGATCGGCAAGTCTGAGGCGGCTATTGCTACTCACTCAAGATCG 634
DB 61 CAACGAACTGTGATCGGCAAGTCTGAGGCGGCTATTGCTACTCACTCAAGATCG 120
QY 635 TGCAAGAACTCTCAAGTGTGAGAACTGTGTTTCTACACCGGCTAAGAACTCGAAGA 694
DB 121 TGCAAGAACTCTCAAGTGTGAGAACTGTGTTTCTACACCGGCTAAGAACTCGAAGA 180
QY 695 TTGTATAGAGTCTTCATCTGCTAAGTAAAGTGGCTATCAAGGAGCCCTGTG 754
DB 181 TTGTATAGAGTCTTCATCTGCTAAGTAAAGTGGCTATCAAGGAGCCCTGTG 240
QY 755 GGACCCCGAGTATCTGGCCCGAG 778
DB 241 GGACCCCGAGTATCTGGCCCGAG 264
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RESULT 11

US-09-579-664B-3

Sequence 3, Application US/09579664B

Patent No. 6514719

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Bird, Timothy A.

APPLICANT: Vrica, G. Duke

APPLICANT: Martin, Unja

APPLICANT: Anderson, Dirk M.

TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

FILE REFERENCE: 2923-A

CURRENT FILING DATE: 2000-05-26

CURRENT APPLICATION NUMBER: US/09/579,664B

NUMBER OF SEQ ID NOS: 36

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SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1694
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-579-664B-3
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Query Match 8.0%; Score 249.2; DB 4; Length 1694;

Best Local Similarity 55.7%; Pred. No. 4.4e-47;

Matches 538; Conservative 0; Mismatches 398; Indels 30; Gaps 2;

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QY 251 ATACAGCGATCGAGGAGCTGACATATATGATTGTGAGCAGGTCATCAAGTCAAGG 310
DB 280 AATAGCAAGCAGAGACATTAAGAAATCTTCAAGTTCAAGAGACCTCGAAGTGGG 339
QY 311 AGTTTGTGAATCTTCGCGGCAAGAGCAAGACAGAGCAAGCTGACACTGCAAGA 370
DB 340 CCTTTTCAAGTTGTTTAAAGCGAGAAAGTACTAGGAGTCTTCGAGTGAAGT 399
QY 371 AGTTCAGAGCGGAGCGCGCAAGGTCGGAAGTCTGCAAGAGAGATAGCATCC 430
DB 400 GCATCCCGAAGAGCGCTGAAGGCAAGAGAGCATGAGAACGAGATTGCCGTC 459
QY 431 TCAAGATGTGAAGATCCCAATCTCAAGCTGTGATGTGTGACCCGCAAG 490
DB 460 TTAGAAAGATTAGATGAAGAAATTTGCTTGAAGATTTATGAAGCCCAATC 519
QY 491 AGTACTTATCTTCCTGAGCTGCGCAGGAGAGGAGTGTGATCTGATCC 550
DB 520 ACCCTACTGTGATGCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
QY 551 AGGCTACTACTCGAGAGAGACACAGCAAGTGTGATCGGCAAGTCTGAGAGCGCTGG 610
DB 580 AGGGGTTTACACAGAGAAAGATGCAAGATCTCATCGGAGGCTCTGATGCGAT 639
QY 611 CCTATTGCACTCACTCAAGATCTGTCACAGAGATCTCAAGTGTGAAGAACTGGTTACT 670
DB 640 ACTATCTCAGAGAAATGGGCAATGTGTCAAGGAGCTCAAGGCGGAGATCTTACT 699
QY 671 ACAACCGGTGAAGAACTGGAATGTGTATGAGATCTCATGCTGCTAAGTAG--- 727
DB 700 ACGTCAAGACAGAGATCTCAAAATATGATAGTATGATCTGTGCTGTGAAGTGAAG 759
QY 728 ---AAATGGCTCTCAACAGAGAGCCCTGTGAGACCCCGAGATCTGAGAGGATG 784
DB 760 GCAAGAGATGTATGTATCCAGGCTGCGGAGCCCGAGCTATGTGCTCGAAGTTC 819
QY 785 TAGGCGGAGGAGATGAGACCCCTGTGATCTGTGAGCTGTGAGCTTGAAGTCAATGAT 844
DB 820 TGCCCGAAGACGTAAGCAAGAAAGTGTGATCTGTGAGCTGTGAGCTTGAAGTCA 879
QY 845 TCTGTGTTCAAGCAATCCACTTTCTATGAGAGTGAAGAAATATATATGGAACC 904
DB 880 TCTGTGTTCAAGCAATCCACTTTCTATGAGAGTGAAGAAATATATATGGAACC 915
QY 905 ATGATTAAGATCTCTCGCAGAGATCTGTGAGTGTGATGATGATGATGATGATGAT 964
DB 916 ATGATTAAGATCTCTCGCAGAGATCTGTGAGTGTGATGATGATGATGATGATGAT 975
QY 965 GGGATGATTTTCGAGAGAGCAAGACCTGTGATCAAGGCTGATGAGAGTGAAGCAAG 1024
DB 976 GGGATGATTTTCGAGAGAGCAAGACCTGTGATCAAGGCTGATGAGAGTGAAGCAAG 1035
QY 1025 ACCAGCGATCACTGCAAGAGAGGCTATCTCAAGTGAAGTGTGCAATGCTGCTT 1084
DB 1036 ATAAAGATACACTGTGTGAGAGAGGCTGACACCCATGATGATGATGATGATGAT 1095
QY 1085 CTGATTAAGAACTCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
DB 1096 TTAGCAAAACATCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1155
QY 1145 AGTGAAGAGGCTGCTGAGTGAACCACTCATGAAAGGCTCGGAGCAAGAGCAT 1204
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Db 1156 AATGAGACAGGCTTTAAAGCCACGCGACGTGCTGAGACATATGCGGAGGCTCCAGCTTG 1215
QY 1205 CCAGCA 1210
Db 1216 GCAGCA 1221

RESULT 12
US-09-230-896C-5
; Sequence 5, Application US/09230896C
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Sutcliffe, et al.
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
; FILE REFERENCE: TSRI-548.1
; CURRENT APPLICATION NUMBER: US/09/230,896C
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 60/023,220
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: ratus ratus
US-09-230-896C-5

Query Match 8.0%; Score 249; DB 4; Length 1458;
Best Local Similarity 55.3%; Pred. No. 4.5e-47;
Matches 539; Conservative 0; Mismatches 405; Indels 27; Gaps 2;
QY 249 CTATTAACAGCCATCGGAGGTGATGACAGATATGATTTGGGACAGGTCACTCAAGCTGA 308
Db 61 CAAAGAAACAGACGAGAGACATCAGAGTGTCTATGAGATCCGGAAGAGCTGGGCTCGGG 120
QY 309 GAGATTTTGAATCTTCCGGCCCAAGACAGACAGACAGAGCTGACACCTGCAA 368
Db 121 TGCTTCTCGAGGTATGTGCGCCAGAGAAAGGCGCTGCTCATCTTGTGGCCCTCA 180
QY 369 GAAATTCAGAGCGGAGCGCGCAAGGTGCGGAAAGCTGCCAAGACGAGATAGGCA 428
Db 181 GTGATTCACAGAAAGACATTCGGGCAAGAGCGCTGTGAGAAATGAGATCGAGT 240
QY 429 CTTCAAGATGTGAAGATCCCAACATCTTACAGCTGTGTGAGATGTTGTGACCCGCA 488
Db 241 ACTCCGAGAGATTAGCCACCACCAATGTGCTCTGAGAGAGTCCACAGAGGCGCTTC 300
QY 489 GGAATCTTATCTTCTGAGCTGGCCACAGGAGGAGGAGTGTGACCTGGA 548
Db 301 CCACTCTTACTTGAGCTGAGAGCTGTGACAGTGTGAGTCTTTGACGAAATCTGA 360
QY 549 CCAAGGCTACTACTCGAGAGAGACACAGCAACGTGTACCGCAAGCTCTGAGGCGGT 608
Db 361 GCGGCGGCTCTTACAGAGAGAGATGAGACCACTTGTAGGCGAGGTCTTGTGTCTGT 420
QY 609 GGGCTATTGCACTCAAGATCTGTGACAGAGATCTCAAGCTGAGAACTGTGTTA 668
Db 421 CTCTTACTTCAATGAGCTGTGGGCAATCGTGACCGGAGCTCAAGCTGAAAACTCTCTTA 480
QY 669 CTCAACCGGCTGAAGACTCGAAGATGTGATCAAGTATTCATCTGCTGAGCTAAGTAA 728
Db 481 TGCCACACCTTTTGAGGACTCCAGATCATGTCTTGTGACTTTGGCTGTCCAAAAATTA 540
QY 729 AATAGCCTCATCAAGA---GCCCTGTGGGACCCCGAGATATCTGACCCCAAGGTGAT 785
Db 541 AGCTGGCAACATGTGAGCAGACAGCTGTGGGACCCAGAGATATGTGGCCCAAGCTCCT 600
QY 786 AGGCGGAGCGGTATGAGAGCGCCCTGTGACTGCTGGGCGCATTTGAGTCACTATGAT 845
Db 601 GAGAGCAAAACCTTACGGAAGGCGGTAGATGTGTGGCCCTGAGTGTCTCTACAT 660
QY 846 CTGCTTTGAGGCAATCACTTTCTATGAGAGGTGGAAGAAATGATTATGAGACCA 905

Db 661 CTTCTGTGTGGATACCCCTTTCTATGATGAGAGGATCCCTGA----- 706
QY 906 TGATAGAAATCTCTTCGCAAGATCTGTGCTGTGATGATGATTTGACTTCCTCATTTG 965
Db 707 -----CTCTTACCCAGATTTCTGAGGCGAGCTACGAGTTTACCTCCCTTTTG 756
QY 966 GATGATATTTCCGAGGACGCAAGACTGTGTCAAGGCTATGAGAGTGAAGCAGA 1025
Db 757 GATGATCATCTCAAAATCAGCAAGACTTCTTCTGAGCACTTCTGAAAGTATCCCA 816
QY 1026 CCAAGGATCATGCAAGAGGAGGATCTCCATGATGATTTCTGCAATGCTGCTTC 1085
Db 817 GAAAGGTTCCTCGCAAGAGGCTTACAGCATCTTGTGATCTTGGGATGAGACTT 876
QY 1086 TGATAGAAATCTCAAGAGTGTGTCTGTGCGCAGATTGAAAGAACTTTGCCAGGCGCA 1145
Db 877 GAGACAGGACATCTTATGTTCTGTCACTGAGCAGATCCAGAAATTTTCCAGAGCCCA 936
QY 1146 GTGAGAGAGGCTGTCCAGTACACCTCTCATGAAAGGCTCCGAGCAGAGCAGTC 1205
Db 937 CTGGAAGGTGATTCATGATGCAATCATCTTCTTACATCCATCCGTAAAGCTGGGACAG 996
QY 1206 CAGCAGGCTG 1216
Db 997 CCAAGAGGTG 1007

RESULT 13
US-09-620-312D-526
; Sequence 526, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyen
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wenman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundang
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillingshaast
; APPLICANT: Drmanac, Radje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc FL_genes Version 1.0
; SEQ ID NO 526
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(1372)
US-09-620-312D-526
Query Match 7.8%; Score 244.8; DB 4; Length 1733;
Best Local Similarity 53.7%; Pred. No. 4.5e-46;
Matches 597; Conservative 0; Mismatches 482; Indels 33; Gaps 3;

QY 108 CGAGGCGAATTTCTGCCCCCGGCGGAGCCCTCGGCGCCCGCTGAGCCCGCATCAC 167
 DB 106 CGAGGCGGAGCGGCGGCGCATCCCCGCGCGCTCTGCGCCGCGCGCGCGCCCGCGCGCG 165
 QY 168 TTCTCTCTCTGACCAACCGCGCGCTGCAAGTTAGAGCTTGGCAATGCCGTTTGGTGTGT 227
 DB 166 CCGTCCCGACCGCGCGCGCGCGCTCTCGGCGCGCGCTCTGCGCGCATGCGCGCGG 225
 QY 228 GACTCTGGGCGAGCAAGAACTTAACAGCCATGCGAGG---TGACTGACGATATGA 284
 DB 226 GAACGCGGAGAGCGCTCTCTGAGAAAAGCAAGCTGAAGACATCAAGAGATCTTCA 285
 QY 285 TTGGGACAGGTCATCAAGACTGAGAGGTTTGGAAATCTTCGGGCGCAAGACAAGAC 344
 DB 286 GTTCAAGAGACCTCGGAGACCGGGGCTTTCCGAAAGTGGTTTACCTGAAGAGAGGC 345
 QY 345 GACAGGCAAGCTGCAACTGCAAGAAATTCCAGAAACCGGAGCGCGCAAGGTGCGGAA 404
 DB 346 AACTGGCAAGCTTTTGTCTGTAAGTGTATCCCTAAGAGAGCGCTGAAGGGCAAGAAAG 405
 QY 405 AGCTGCCAAGACAGATAGGCAATCTCAAGATGTTGAAGCATCCCAATCCTACAGCT 464
 DB 406 CAGCATGAGAAATGATAGCGGCTGCTGAGAAAGATTAGCAATGAATAATTGTGCGCT 465
 QY 465 GGTGGAATGTTGTGACCCGCAAGAGTAATTATCTCTGAGAGCTGCCACGGGGAG 524
 DB 466 GGAAGACATTTATGAAGCCCAATCACTGTACTTGTATGATGAGTGTGTGCGGTG 525
 QY 525 GGAAGTGTGACTGATCTCTGAGACGAGGCTACTACTCGGAGCGAGACAAGCAAGT 584
 DB 526 AGAGCTGTGTAACCGGATAGTGAAGAGGGTTTATACAGAAAGATGCCAGACTCT 585
 QY 585 GGTACGCAAGTCTGAGAGCGGCTGCTTATTTGCACTCACTCAAGATGCTGACAGAA 644
 DB 586 GATCCGCAAGTCTGAGCGCGGTGACTATCTCAAGATGGGCAATGCTCCACAGAGA 645
 QY 645 TCTCAAGCTGAGAACTGTTTACTACACCGGCTGAAGAACTCCAAAGTTGTCATCAG 704
 DB 646 CCTCAAGCGCCGAAATCTCTGTACTACAGTCAAGATGAGAGAGTCCAAATTAATGATCAG 705
 QY 705 TGACTTCATCTGGCTAAGCTAG-----AAATGCGCTCATCAAGAGCGCGTGGGAG 758
 DB 706 TGACTTTGATTTGCAAAATGAGGGCAAGAGATGTATGTCATCTGCTGTGAAAC 765
 QY 759 CCGCGAGTATCGGCGCCAGAGGTGTAGCGCGGACGCGATGAGACGCCCTGTGACTG 818
 DB 766 TCCAGGCTATGTGGCTCTCTGAAATCTCGCCCAAAACCTTACAGCAAAAGCGTGACTG 825
 QY 819 CTGGGCGCATTTGAGTATCATGATCATCTCTGCTTTCAGGCAATCACTTTCTATGAGGA 878
 DB 826 CTGGTCAATCGGAGTGAATGCTTACATCTTGTCTGCGGCTACCTCTCTT----- 876
 QY 879 GGTGGAAGAAATGATATGGAACCATGATTAATAATCTCTTCGCAAGATCTGCTG 938
 DB 877 -----TTATGATGAATAATGATCTCAAGCTCTTTGAGCAGATCTCTCAAGGC 921
 QY 939 TGACTATGATTTGATCTCTCATATTTGGGATGATATTTGCGAGGCGCAAGACCTGAT 998
 DB 922 GGAATATGAGTTTATCTCTCTCTGATGATGATCTTCGCACTCTCAAAAGACTTTCAT 961
 QY 999 CACAGGCTGATGAGAGGTGAGCAAGACAGCGGATCACTGACAGAAAGGCGCATCTTCCA 1058
 DB 982 TCGGAACCTGATGAGAGAGCCCGAATTAAGATACAGTGTGAGAGGAGAGTGGCGCA 1041
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 DB 1162 GAGACATATGAGAAAACTACACTTCGCGACCA 1193

RESULT 14
 US-08-989-12
 / Sequence 12, Application US/08878989
 / Patent No. 5885803
 / GENERAL INFORMATION:
 / APPLICANT: Bandman, Olga
 / APPLICANT: Hillman, Jennifer L.
 / APPLICANT: Corley, Neil C.
 / APPLICANT: Guegler, Karl G.
 / APPLICANT: Lal, Preeti
 / APPLICANT: Goli, Surya K.
 / APPLICANT: Shah, Puri
 / TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 / NUMBER OF INVENTION: KINASES
 / NUMBER OF SEQUENCES: 21
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Incyte Pharmaceuticals, Inc.
 / STREET: 3174 Porter Drive
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/878, 989
 / FILING DATE:
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Billings, Lucy J J
 / REGISTRATION NUMBER: 36,749
 / REFERENCE/DOCKET NUMBER: PF-0321 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415-855-0555
 / TELEFAX: 415-845-4166
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 12:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1282 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: PROSNOT06
 / CLONE: 827431
 / US-08-878-989-12

Query Match 7.8%; Score 242.6; DB 2; Length 1282;
 Best Local Similarity 55.3%; Pred. No. 1.2e-45;
 Matches 529; Conservative 0; Mismatches 400; Indels 27; Gaps 2;

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 QY 311 AGTTTGTGAATCTTTCGGGCGCAAGACAGACAGCAAGCAAGCTGCAACCTGCAAGA 370
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RESULT 15
US-09-272-796-12
Sequence 12, Application US/09272796
Patent No. 6207148

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lai, Preeti
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT06
CLONE: 827431
US-09-272-796-12
Query Match 7.8%; Score 242.6; DB 3; Length 1282;
Best Local Similarity 55.3%; Pred. No. 1.2e-45;
Matches 529; Conservative 0; Mismatches 400; Indels 27; Gaps 2;
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DB 754 AGCAGAAACCCCTACGGGAAAGCCGTAGATGTGTGGCCCTGGGCGTCATCTCTACATCC 813
QY 848 TGCTTCAGGCAATCCACCTTTCTATGAGAGAGTGAAGAAGATGATATGAGAAACATG 907
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QY 908 ATAGATCTCTTCCGCAAGATCCTGTGCTGACTATGATGATTTGACTCTCCATATTGG 967
DB 858 -----CTTCAGGCAATCTGTAGGGCCAGCTATGAGTTTGACTTCTCTTCTGG 909
QY 968 ATGATATTTCGAGGAGACCCAAAGACCTGTGTCAGAAAGCTGATGAGGTGAGCAAGACC 1027
DB 910 ATGACATCTCAGATCAGGCAAGAACTTATGTGGACCTTCTGGAGCGAGACCTTCAGA 969
QY 1028 AGCGATCACTGCAAGAGGCCATCTCCATGATGATTTCTGGCAATGCTGCTTCTG 1087
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Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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5	3018.8	96.6	3022	BD127328	BD127328 Primer fo
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8	3000.8	96.1	3017	AX680150	AX680150 Sequence
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10	2999.8	96.0	3003	BC005828	BC005828 Homo sapi
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ALIGNMENTS

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DEFINITION	Sequence 1 from patent US 6461846.				
ACCESSION	AR235862				
VERSION	AR235862.1	GI:27279200			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 3124)				
TITLE	Yan, C., Wei, M.-H., Ketchum, K., Merkulov, G. and Beasley, E.M.				
JOURNAL	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof				
	Patent: US 6461846-A 1 08-OCT-2002;				

FEATURES
source

Location/Qualifiers
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/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 3124; DB 6; Length 3124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2701	ATTTTGTGCTCAGTTCACAAATGAATGAAGAGAACTCCCTCTTTCTACAGCTCACTTC	2760
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QY	2761	TATCAGAGGCCAGGTGCTCAGAGCCACATTAAGTGTCTTTTCTGAGATGAGAAAGTA	2820
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VERSION AX350342.1
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1 Yan, C.C., Wei, M.H., Ketchum, K.C., Merkulov, G.C. and Beasley, E.M.
Isolated human kinase proteins, nucleic acid molecules encoding
human kinase proteins, and uses thereof
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JOURNAL Applera Corporation Robert A. Millman Assistant Secretary (US)
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AUTHORS	1 (bases 1 to 3057)				
	Klauser, R.D., Collins, F.S., Wagner, K.H., Schaefer, C.F., Bhat, R.K.,				
	Altschul, S.F., Zeeberg, B., Bietow, K.H., Schaefer, C.F., Bhat, R.K.,				
	Hopkins, R.F., Jordan, H., Moore, T., Wax, S.L., Wang, J., Hsieh, F.,				
	Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.W., Hong, L.,				
	Scapleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L.,				
	Schaefer, T.E., Brownstein, M.J., Ushin, T.B., Toshiyuki, S.,				
	Carninci, P., Prange, C., Raha, S.S., Locantello, N.A., Peters, G.J.,				
	Abramson, R.D., Mulian, S.J., Bosak, S.A., McEwen, P.J.,				
	McEwen, R.D., Malek, J.A., Gunaratne, P.H., Richards, S.,				
	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,				
	Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,				
	Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,				
	Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,				
	Boffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,				
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TITLE
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
MEDLINE
22388257
12477932
2 (bases 1 to 3057)
Strausberg, R.
TITLE
Direct Submission
Submitted (13-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Issue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Rita Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natafja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 6 Row: 1 Column: 12
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ORIGIN

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3022)
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AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 2759 22-JAN-2002;
HELIIX RESEARCH INSTITUTE
OS Home sapiens (human)
PN JP 2002017375-A/2759
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC

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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (194)..(1696).

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 REFERENCE
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 Authors
 Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
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 Kawai, H., Y., Saito, K., Yamamoto, J., Makamatsu, A., Nakamura, Y.,
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 NEDO human cDNA sequencing project
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 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kibetaru, Chiba 292-0812, Japan
 (E-mail: genomics@nri.co.jp, Tel: 81-438-52-3575, Fax: 81-438-52-3586)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology; cDNA library construction:
 Institute of Medical Science, University of Tokyo; Laboratory of
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Thu Apr 29 08:44:17 2004

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 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
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 Contact: nisc.mgc@nih.gov
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 Generation and initial analysis of more than 15,000 full-length
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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 Contact: MGC help desk
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 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@cgsc.bc.ca
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3176)
AUTHORS Hambrecht, R., Heubner, D., Mewes, H.W., Weill, B., Amid, C., Oesterger, A.,
Fodor, G., Han, M. and Wiemann, S.
The German Human cDNA Consortium
Direct Submission
JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberberg, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686D0882) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.
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Db      2401  GGTATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
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Db      2461  AAGCTTCCATTTTGTCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520

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RESULT	13
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LOCUS	2923 bp DNA linear PAT 09-MAR-2001
DEFINITION	Sequence 230 from Patent WO0112659.
ACCESSION	AX086278
VERSION	AX086278.1 GI:13275924
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 Wiemann S. Human dna sequences Patent: WO 0112659-A 230 22-FEB-2001; German Human Genome Project (DB) Location/Qualifiers 1..2923 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
TITLE	
JOURNAL	
FEATURES	
source	
ORIGIN	
Query Match	90.4%; Score 2824.2; DB 6; Length 2923;
Best Local Similarity	97.1%; Pred. No. 0
Matches 2920; Conservative	0; Mismatches 3; Indels 84; Gaps 1

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QY	109	GGAGCGGATTTGACCCCGCGCTCCCGGAGCCCTCGGCGCCCGCTGAGCCCGCATCACT	168
Db	61	GGAGCGGATTTGACCCCGCGCTCCCGGAGCCCTCGGCGCCCGCTGAGCCCGCATCACT	120
QY	169	TCTCTCCTGTGACCAACCGGCGCTGCAAGTTAAGCTTGCCATATGCCGTTTGGGTGTG	228
Db	121	TCTCTCCTGTGACCAACCGGCGCTGCAAGTTAAGCTTGCCATATGCCGTTTGGGTGTG	180
QY	229	ACTCTGGGCGACAAAGAAAGACTTAACAGCCATCGAGGTGACTGACAGATATGATTTG	288
Db	181	ACTCTGGGCGACAAAGAAAGACTTAACAGCCATCGAGGTGACTGACAGATATGATTTG	240
QY	289	GGAAGGTTCATCAAGACTGAGAGTTTGTGAATCTTCCGGGCGAAGACAAGCAGACA	348
Db	241	GGAAGGTTCATCAAGACTGAGAGTTTGTGAATCTTCCGGGCGAAGACAAGCAGACA	300
QY	349	GCGAAGCTGCAACACTGTCAGAAAGTTCCAGAACCGGCGGCAAGGTGCCGAAAGCT	408
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QY	409	GCCAAAGACGAGATAGGSCATCTCAAGATGAGTGAAGATCCCAATCTTACAGCTGTG	468
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QY	469	GATGTGTTTGTGACCCGCGAAGAGTACTTATCTCTCGAGCTGCGCACGGGAGGAG	528
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QY	529	GTTGTTGACTGATCCTGACCCAGGCTACTACTCGAGCGAGACACAAGCAACTGTGTA	588
Db	481	GTTGTTGACTGATCCTGACCCAGGCTACTACTCGAGCGAGACACAAGCAACTGTGTA	540
QY	589	CGGCAATCCTCGAGGCGCGTGCCTATTGCACTCACTCAAGATCGGACAGGAATCTC	648
Db	541	CGGCAATCCTCGAGGCGCGTGCCTATTGCACTCACTCAAGATCGGACAGGAATCTC	600
QY	649	AAGCTGAGAAACCTGATTTACTCAACCCGCTGAGAACTCGAAGATTGTCACTAGTAC	708
Db	601	AAGCTGAGAAACCTGATTTACTCAACCCGCTGAGAACTCGAAGATTGTCACTAGTAC	660
QY	709	TTCATCTGGCTAAGCTAAGAAATGGCTCATCAAGAGCCCTGTGGACCCCGAGTAT	768
Db	661	TTCATCTGGCTAAGCTAAGAAATGGCTCATCAAGAGCCCTGTGGACCCCGAGTAT	720
QY	769	CTGGCCCCAGAGGTGTAGGCCGCGACCGGTATGAGCCCTGTGACTGTGGCCATT	828
Db	721	CTG-----	723
QY	829	GGAATCATCATATGATCTGCTTTGAGGCAATCACTTCTATGAGAGGTGAAGAA	888
Db	724	-----GGCAACCACTTTCTATGAGAGGTGAAGAA	756
QY	889	GATGATTATGAAACCATGATPAGAAATCTTTCGCAAGATCTGGCTGTGACTATAG	948
Db	757	GATGATTATGAAACCATGATPAGAAATCTTTCGCAAGATCTGGCTGTGACTATAG	816
QY	949	TTTGAATCTCCATATTGGAGTATATTTCGAGGACGCCAAAGACTGTGTCAAGGCTG	1008
Db	817	TTTGAATCTCCATATTGGAGTATATTTCGAGGACGCCAAAGACTGTGTCAAGGCTG	876
QY	1009	ATGAGAGTGAAGACCAAGCGGATCACTGACAAAGAGGCGCATCTCCATGAGTGATT	1068
Db	877	ATGAGAGTGAAGACCAAGCGGATCACTGACAAAGAGGCGCATCTCCATGAGTGATT	936
QY	1069	TCTGGCAATGCTGCTTCTGATPAGAAACATCAAGAGTGTGTCTGTGCCAGATTGAAG	1128
Db	937	TCTGGCAATGCTGCTTCTGATPAGAAACATCAAGAGTGTGTCTGTGCCAGATTGAAG	996
QY	1129	AACTTTGCAGAGCGCAAGTGAAGAGGCTGTCCGAGTACCACTCTATGAACCGCTC	1188

Db 997 AACTTTGCCAGGGCCAGATGGAAGAGGCTGTCCAGATGACCACTCTCATGAACGGCTT 1056
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Db 1057 CGGGCACAAGAGCAGTCCAGCACGGCTGCAAGCCAGTCCGCTCAGCCACAGACACTGTC 1116
Qy 1249 ACCCCCGGGGCTGAGGTGGGGCCACAGCTGCAAGCTGCGAGTGAAGTACTCAGCCCT 1308
Db 1117 ACCCCCGGGGCTGAGGTGGGGCCACAGCTGCAAGCTGCGAGTGAAGTACTCAGCCCT 1176
Qy 1309 GAGGGTATGCTGTCTGTCTGCAAGAGTAAATGTGCCCCCGGAGCCCTATGTGC 1368
Db 1177 GAGGGTATGCTGTCTGTCTGCAAGAGTAAATGTGCCCCCGGAGCCCTATGTGC 1236
Qy 1369 ACCCCAGCCACAGATGAGATGCCCCAGCCACTGATGGCAGTGTCACTCCAGCCACC 1428
Db 1237 ACCCCAGCCACAGATGAGATGCCCCAGCCACTGATGGCAGTGTCACTCCAGCCACC 1296
Qy 1429 GATGGAAGCATCACTCCAGCCACTGATGGAGTGTCACTCCAGTCACTGAAGAGCGCT 1488
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Db 1417 CAAGAGCATGTCATGTGGGCCACCAAGGCGCTGCCACCCCTAGCGGGTATGGCCAG 1476
Qy 1609 CCGGACAGCACAAGCCCCAGAGGGCGCCACAGGCGCTCCACTCTAGTAAAGGGAGA 1668
Db 1477 CCGGACAGCACAAGCCCCAGAGGGCGCCACAGGCGCTCCACTCTAGTAAAGGGAGA 1536
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Db 1537 GAGGCTGTGTTATGCTCCAGAGTCTCAAGAGAGAGGCGCAGTGAAGGCACTG 1596
Qy 1729 GTAGAGGGGGGAGGAGATGGGCAAGAGGGTGGAGAGTGAAGAGGGGTTTCACTGT 1788
Db 1597 GTAGAGGGGGGAGGAGATGGGCAAGAGGGTGGAGAGTGAAGAGGGGTTTCACTGT 1656
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Db 1657 ACATAGAGTCACTGGAGTGAATGCGCTGCCCTCCAGCCCAATCCAGTGGGAGCAT 1716
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Qy 1909 GGGCAGTGGAGGGGCGGGCCCAAGCCCCCTGCAATGATCTTGTGTGCTTTTCTTT 1968
Db 1777 GGGCAGTGGAGGGGCGGGCCCAAGCCCCCTGCAATGATCTTGTGTGCTTTTCTTT 1836
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Qy 2209 CTCTAGAGCAGATACAGGCTGTATAGAGATCAGAAAGTATAGGCACTATGTTTAA 2268

Db 2077 CTCTAGAGCAGATACAGGCTGTATAGAGATGCAGAAAGTATAGGCGCATGTTAA 2136
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Db 2137 TTCAGACTTTGGCAATGGCTTAGGAAATCTGCTCACTAGCTGTGAGGTCTCAGAGTGG 2196
Qy 2329 AGAAGATAGTATAGAGGGGCAAGAGCTTCCATTTTGTCTCTCTAAGACCTGTATTG 2388
Db 2197 AGAAGATAGTATAGAGGGGCAAGAGCTTCCATTTTGTCTCTCTAAGACCTGTATTG 2256
Qy 2389 TGTATTTTCTGCTCTTCCAGAGTCCCTGAGTGGGCTGCTGACCTGAACTCATAG 2448
Db 2257 TGTATTTTCTGCTCTTCCAGAGTCCCTGAGTGGGCTGCTGACCTGAACTCATAG 2316
Qy 2449 CCTTAAAGGAAAGAGGAAATTAAGACCTGAGCAGTGAAGCTGGCAGAGGATAC 2508
Db 2317 CCTTAAAGGAAAGAGGAAATTAAGACCTGAGCAGTGAAGCTGGCAGAGGATAC 2376
Qy 2509 AAGCCAGACCCAGTGTCCAGGCTTACTGTGGTCTTACCTTGGGCCAAACAGGAGGG 2568
Db 2377 AAGCCAGACCCAGTGTCCAGGCTTACTGTGGTCTTACCTTGGGCCAAACAGGAGGG 2436
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Db 2437 CTGATACCTCTTGTCTCTCTAGATGCCCACTCTTACATCTCAGGCCCAAGTCTC 2496
Qy 2629 TCCACCTTAAAGGAGGCTTCTGCTCATAGCAGTAATCTATCTGATTTGAGGTTGGCT 2688
Db 2497 TCCACCTTAAAGGAGGCTTCTGCTCATAGCAGTAATCTATCTGATTTGAGGTTGGCT 2556
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Db 2557 TTACAGGGGAGATTTTCTGCTCAATTCATGAAATGAAGAGAACTCCTTTCT 2616
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Qy 2809 GATGAGGAAGTATAGGTTAACTCCCAAGTTTCCAGAGGAGGCTCCAGAGTGGCTT 2868
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Qy 2869 TGTCAAGCCTTACCAAGCCTGATAGGAGCAGCCATTTGCTCTGCGCTTGGAC 2928
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Qy 3049 AAAAAA 3055
Db 2917 AAAAAA 2923

RESULT 14
LSM801665
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

HSN801665 2923 bp mRNA linear PRI 20-MAR-2002
Homo sapiens mRNA; cDNA DKFZp564E0482 (from clone DKFZp564E0482);
complete cds.
AL136697
AL136697.1 GI:12052915
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2923)
Poustka, A., Klein, M., Mewes, H. W., Gassenhuber, J. and Wiemann, S.

Db	1237	ACCCAGACCAAGATGAGAAAGTGCCACCCAGACCACTGATGGCAAGTGCACCCAGGCACC	1296
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Db	1357	ACTCCAGCACTGATGAGGAGGCCACACACGCCACAGAAAGAGACACTGTGCCACACC	1416
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QY	1609	CCGAGACAGCACAGCCCCAGAGGGGCGCCACAGGCCAGGCTCCACCTCTTAATAAGGGAA	1668
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QY	1669	GAGCGCTGTGGTTATGCCAGAGTCTTAAAGGAGAGGGCAGCTGATGATGAGGAGCGCTG	1728
Db	1537	GAGCGCTGTGGTTATGCCAGAGTCTTAAAGGAGAGGGCAGCTGATGATGAGGAGCGCTG	1596
QY	1729	GTGAGGGGGGGGCAAGGGATGAGGCGAGAGGGTGGAGAGATGATGAGAGGGGCTTCACTGT	1788
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QY	1909	GGCCAGTGGGCAAGGGCGCGGCCGCCAGCCCTGCAATGGATTCCTGTAGGCTTTCTGTCTTT	1968
Db	1777	GGCCAGTGGGCAAGGGCGCGGCCGCCAGCCCTGCAATGGATTCCTGTAGGCTTTCTGTCTTT	1836
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QY	2089	CACACTCTCCCAAGGCGCTTAAATTGGGGGGCGCTTGCCTGAAAGGTGTCTCCCAAGCAG	2148
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QY	2149	GCCCTGTAGCGGCTTATAGGCTCTCTGCACTAATAAGTGTGTCTGTAGTGTGGGCTG	2208
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QY	2389	TGTTATTTCTCTGCTTCCGAGTCTCGACGTGGGCTGCCCTTACCTGAACCTCATGAG	2448
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QY	2569	CTGATACCTCCTTGTCTCTTCTAGATGAGCCACCTCTTACATCTCAGGCCAGAGTCTCT	2628
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Db	2497	TCCACCTTACGGGGCTTGTCTGATAGGCAATGACATATCTGATTGAGGTTGCGCT	2556
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Db	2557	TTACAGGGGCGAGATTTTCTGTCTCAGTTCAACATGAATGAGGAACCTCCCTTTCT	2616
QY	2749	ACAGCTACCTTCATCAGAGGCCAGGTGCTCAGAGCCACATTAAGTTGCTTTTCTGG	2808
Db	2617	ACAGCTACCTTCATCAGAGGCCAGGTGCTCAGAGCCACATTAAGTTGCTTTTCTGG	2676
QY	2809	GATAGGAGAGTGGGTTAACTCCCGAGTTTCTGAGGAGGCTCCTGACAGTGGCCTT	2868
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QY	2869	TGTGAGACCTTACGACAGCGCTGATATGAGGAGCCACATTTGTCCTGCGCTTGCGGAC	2928
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Db	2917	AAAAAA 2923	
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LOCUS	BD127354	2905 bp	DNA linear PAT 18-SEP-2002
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD127354		
VERSION	BD127354.1	GI:23222299	
KEYWORDS	JP 2002017375-A/2785.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 2905)		
	Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,		
	Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and		
	Koga,H.		
TITLE	Primer for synthesizing full-length cDNA and use thereof		
JOURNAL	Patent: JP 2002017375-A 2785 22-JAN-2002;		
COMMENT	HELIX RESEARCH INSTITUTE		
	OS Homo sapiens (human)		
	PN JP 2002017375-A/2785		
	PD 22-JAN-2002		
	PF 07-JUL-2000 JP 2000253172		
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	PI ISHII,		
	PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI		
	PI SHINICHI KOJIMA,		
	PI TETSUJI OTSUKI,HISASHI KOGA		
	PC		
	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC		
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	PC C12P21/02,C12Q1/68//C12P21/08,G06F7/30,C12N15/00,C12N5/00 CC		

Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (164)..(1573).
Location/Qualifiers
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/mol_type="Genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 89.4%; Score 2792.4; DB 6; Length 2905;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2899; Conservative 0; Mismatches 6; Indels 93; Gaps 1;

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108 CGAGAGGAGATTCTGCGCCGCTCTCCCGGAGCCCTCGAGCCCGCGCGTCTGAGCCCGGATGAC
61 CGAGAGGAGATTCTGCGCCGCTCTCCCGGAGCCCTCGAGCCCGCGCGTCTGAGCCCGGATGAC
168 TTCTCTCTCTGTGACCAACCGCGCGCTGACGATTAGAGCTTGCAATGCCGTTTGGGTGT
121 TCCCTCCCTGTGACCAACCGCGCGCTGACGATTAGAGCTTGCAATGCCGTTTGGGTGT
228 GACTCTGGCGGACAGAGAAATCTTACCAAGCATCGAGGTGATGACATGATGATT
181 GACTCTGGCGGACAGAGAAATCTTACCAAGCATCGAGGTGATGACATGATGATT
288 GGGACAGGTCATCAAGACTGAGAGAGTTTGTGAAATCTTCCGGGCAAGACAAAGACGAC
241 GGGACAGGTCATCAAGACTGAGAGAGTTTGTGAAATCTTCCGGGCAAGACAAAGACGAC
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1201 CACCCCGGGGCT----- 1213
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1214 -----GCAAGCCGTAGTGC 1227
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1428 CGATGAGATCACTCTCAAGCACTGATGAGGATGCACTCCAGCACTGATGAGGATGCACT 1487
1288 CGATGAGATCACTCTCAAGCACTGATGAGGATGCACTCCAGCACTGATGAGGATGCACT 1347
1488 TACTCCAGCACTGATGAGGATGCACTCCAGCACTGATGAGGATGCACTCCAGCACTGAT 1547
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Thu Apr 29 08:44:17 2004

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Page 29

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QY 2028 CTTGCTCTCCCTTCCCTTCCCTTCTGCTCAACATTCCTTAGGAGGAGGCTGAGGTC 2087
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 22:03:09 ; Search time 1165 Seconds
(without alignments)
11391.735 Million cell updates/sec

Title: US-10-669-689-1
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
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9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2999.2	96.0	3017	4	AAAD18832 Human kin
4	2824.2	90.4	2923	5	ABX71280 Human sig
5	2792.4	89.4	2905	4	AAK94325 Human ful
6	2791.2	89.3	2840	4	AA158144 Human ful
7	2791.2	89.3	2840	8	ADB48110 Novel hum
8	2790.8	89.3	2897	4	AAAF30481 Human pro
9	2595.2	83.1	2747	4	AA158143 Human pol
10	2595.2	83.1	2747	8	ADB48109 Novel hum
11	2283.4	73.1	2297	5	AAH78261 Nucleotid
12	1956.2	62.6	2494	4	AAK94614 Human ful
13	1876.6	60.1	3915	4	AA527718 DNA encod
14	1876.6	60.1	3915	9	ADB94521 Novel hum
15	1876.6	60.1	7542	6	ABA95683 Human pro
16	1602	51.3	1642	6	AAV73694 CatDanyl
17	1474.6	47.2	1475	3	AAAC59122 Human sec
18	1473.6	47.2	1475	4	AAAD08347 Human sec
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23	850	27.2	862	6	ABK34751 Human CDN

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25	743.2	23.8	896	4	AAK93790 Human CDN
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28	706	22.6	741	4	AAK91953 Human CDN
29	660.2	21.1	768	4	AA195905 Human neu
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31	635.8	20.4	765	4	AA195904 Human neu
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38	497.8	15.9	658	4	ABK43847 DNA encod
39	487.8	15.9	658	9	ADB93362 Human CDN
40	493.6	15.8	599	4	AAK94033 Human CDN
41	493.6	15.8	599	4	AAK92672 Human CDN
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44	447.4	14.3	458	4	AAK93084 Human CDN
45	412.4	13.2	460	8	ACH14155 Human acu

ALIGNMENTS

RESULT 1	ABK95682	ABK95682 standard; CDNA; 3124 BP.
ID	XX	ABK95682;
AC	XX	03-APR-2002 (first entry)
DT	XX	Human protein kinase coding sequence.
DE	XX	Human protein kinase coding sequence.
XX	XX	Human; protein kinase; enzyme; gene; brain; lung; hippocampus;
KW	XX	calmodulin-binding kinase; gene therapy; chromosome 3; ss.
XX	XX	
OS	XX	Homo sapiens.
XX	XX	
PH	XX	Key
FT	XX	Location/Qualifiers
FT	XX	211..1716
FT	XX	/*tag= a
FT	XX	/product= "Human protein kinase"
XX	XX	
PN	XX	W0200192492-A2.
XX	XX	
PD	XX	06-DEC-2001.
XX	XX	
PF	XX	30-MAY-2001; 2001MO-US017327.
XX	XX	
PR	XX	30-MAY-2000; 2000US-0207281P.
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PR	XX	12-DEC-2000; 2000US-00734030.
XX	XX	
PA	XX	(APPL-) APPLERA CORP.
XX	XX	
PI	XX	Yan C, Wei M, Ketchum K, Merkulov G, Beasley EM;
XX	XX	
DR	XX	WPI; 2002-097770/13.
XX	XX	
DR	XX	P-SDB; AAM48279.
XX	XX	
PT	XX	New calmodulin-binding kinase peptides and nucleic acid encoding the
XX	XX	peptides, useful as models for developing human therapeutic targets or in
XX	XX	screening for compounds that modulate kinase.
XX	XX	
PS	XX	Claim 4; Fig 1; 75pp; English.
XX	XX	
CC	XX	The present sequence is the coding sequence for a human protein kinase
XX	XX	and adult brain; lung and hippocampus. The protein kinase is related to
XX	XX	the calmodulin-binding kinase subfamily. The protein kinase and its

CC coding sequence can be used as models for the development of human
CC therapeutic targets, in the identification of therapeutic proteins, and
CC serve as targets for the development of human therapeutic agents that
CC modulate kinase activity in cells and tissues that express the kinase. In
CC addition, the protein kinase coding sequence can be used for treating a
CC disorder associated with nucleic acid expression of the kinase gene,
CC particularly biological and pathological processes that are mediated by
CC the kinase in cells and tissues that express it, as antisense constructs
CC to control kinase gene expression in cells, tissues or organisms, and in
CC gene therapy. The protein kinase gene maps to chromosome 3

XX Sequence 3124 BP; 731 A; 861 C; 897 G; 635 T; 0 U; 0 Other;

Query Match 100.0%; Score 3124; DB 6; Length 3124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GCCCGCGCTCCCGAGCCCTCGCGCGCGCTGCGCGCGCGATCACTTCTCCCTGTGA 180
Db 121 GCCCGCGCTCCCGAGCCCTCGCGCGCGCTGCGCGCGCGATCACTTCTCCCTGTGA 180
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 XX
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 XX
 DT 06-NOV-2001 (first entry)
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 DE Human full-length cDNA, SEQ ID NO: 2956.
 XX
 KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-0018774.
 PR 02-MAY-2000; 2000JP-00183765.
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 XX PA
 PI Ota T, Nishikawa T, Isegai T, Hayashi K, Iehi S, Kawai Y;
 PI Wakematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2001-524255/58.
 DR P-PSDB; AAM93379.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their use
 in genetic manipulation.
 PS Claim 8; SEQ ID NO 2956; 1380bp + Sequence Listing; English.
 CC The invention relates to primers for synthesizing full length cDNA
 clones. 830 cDNA molecules encoding a human protein have been isolated
 and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 been determined. Primers for synthesizing the full length cDNA are useful
 for clarifying the function of the protein encoded by the cDNA. The full
 length clones were obtained by construction of full length enriched cDNA
 libraries that were synthesised by the oligo-capping method. The primers
 enable the production of the full length cDNA easily without any special
 methods. The present sequence is a full length human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 the printed specification, but was obtained in CD-ROM format directly
 from EPO
 XX
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 Best Local Similarity 99.9%; Pred. No. 0;
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Qy 138 CCTCGGG 197
Db 121 CCTCGGG 180
Qy 198 TTAGAGCCTGGCAATGCCGTTTGGGTGTGTGACTCTGGGCGCAAGAAGAACTATTAACA 257
Db 181 TTAGAGCCTGGCAATGCCGTTTGGGTGTGTGACTCTGGGCGCAAGAAGAACTATTAACA 240
Qy 258 GCCATCGAGGTGACTGACATATGATTTGGGACAGGTTCATCAAGCTGAGAGGTTTG 317
Db 241 GCATCGGAGGTGACTGACATATGATTTGGGACAGGTTCATCAAGCTGAGAGGTTTG 300
Qy 318 TGAATCTTCCGGGGCCAAAGACAAAGCAAGGCAAGCTGCAACCTGCAAGAGTTTCA 377
Db 301 TGAATCTTCCGGGGCCAAAGACAAAGCAAGGCAAGCTGCAACCTGCAAGAGTTTCA 360
Qy 378 GAAGCGGGAGCGCGCGCAAGGTGCGGAAAGCTGCCAAGAACAGATAGGATCTTCAAGAT 437
Db 361 GAAGCGGGAGCGCGCGCAAGGTGCGGAAAGCTGCCAAGAACAGATAGGATCTTCAAGAT 420
Qy 438 GGTGAAGCATCTCCCAACATCTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 497
Db 421 GGTGAAGCATCTCCCAACATCTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy 498 TATCTTCTCTGAGAGCTGCGCAGCGGGAGAGAGGTGTTTGACTGGATCTTGGACAGGGCTA 557
Db 481 TATCTTCTCTGAGAGCTGCGCAGCGGGAGAGAGGTGTTTGACTGGATCTTGGACAGGGCTA 540
Qy 558 CTACTCGGAGCGAGACAAAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 617
Db 541 CTACTCGGAGCGAGACAAAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 618 GCACTCACTCAAGATGTGCACAGGAATCTCAAGCTGGAGAACCTGTGTGTGTGTGTGTGTGTGT 677
Db 601 GCACTCACTCAAGATGTGCACAGGAATCTCAAGCTGGAGAACCTGTGTGTGTGTGTGTGTGTGT 660
Qy 678 GGTGAAGAACTCGAAGATGTGCATCAGTGAATCTTCAATCGCTTAAGCTTAAGAAATGGGCT 737
Db 661 GGTGAAGAACTCGAAGATGTGCATCAGTGAATCTTCAATCGCTTAAGCTTAAGAAATGGGCT 720
Qy 738 CATCAAGAGCCCTGTGGAGCCCGCGAGATCTGTGGCCCGAGAGGTGTGTGTGTGTGTGTGTGT 797
Db 721 CATCAAGAGCCCTGTGGAGCCCGCGAGATCTGTGGCCCGAGAGGTGTGTGTGTGTGTGTGTGT 780
Qy 798 GTATGAGAGCCCTGT 857
Db 781 GTATGAGAGCCCTGT 840
Qy 858 CATCAACCTTCTATAGAGAGGTGGAAGAAGATGATTAAGAAACATGATTAAGATCT 917
Db 841 CATCAACCTTCTATAGAGAGGTGGAAGAAGATGATTAAGAAACATGATTAAGATCT 900
Qy 918 CTTCGCAAGATCTGT 977
Db 901 CTTCGCAAGATCTGT 960
Qy 978 GCAAGAGAGCCAAAGACCTGT 1037
Db 961 GCAAGAGAGCCAAAGACCTGT 1020
Qy 1038 TGCAGAGAGGCGCATCTCCATGATGATTTCTGGCAATGCTGCTTGTGATTAAGATCT 1097
Db 1021 TGCAGAGAGGCGCATCTCCATGATGATTTCTGGCAATGCTGCTTGTGATTAAGATCT 1080
Qy 1098 CAAGAGATGT 1157
Db 1081 CAAGAGATGT 1140
Qy 1158 TGTCCAGATGACACCTTATGAAAGGCTCGGGGCAACAGAGAGTCCAGACGCGCTGC 1217
Db 1141 TGTCCAGATGACACCTTATGAAAGGCTCGGGGCAACAGAGAGTCCAGACGCGCTGC 1200

Qy 1218 AGCCAGTGGGCGCTCGAGCCAGACAGACTGCAACCCCGGGGCTGAGAGTGGGGCCACAGC 1277
Db 1201 AGCCAGTGGGCGCTCGAGCCAGACAGACTGCAACCCCGGGGCTGAGAGTGGGGCCACAGC 1260
Qy 1278 TGCAGTGGGAGTGAAGTCACTTCAAGCCCGTGAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1337
Db 1261 TGCAGTGGGAGTGAAGTCACTTCAAGCCCGTGAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
Qy 1338 TGAATGTGG 1397
Db 1321 TGAATGTGG 1380
Qy 1398 AGCCAGTGAAGTGAAGTCAACCCAGCCAGCCAGATGGAAGATCACTCCAGCCACTGATG 1457
Db 1381 AGCCAGTGAAGTGAAGTCAACCCAGCCAGCCAGATGGAAGATCACTCCAGCCACTGATG 1440
Qy 1458 GAGTGTCAACCCAGTCACTGACAGAGCGCTACTCCAGCCACTGATGAGAGACCAACC 1517
Db 1441 GAGTGTCAACCCAGTCACTGACAGAGCGCTACTCCAGCCACTGATGAGAGACCAACC 1500
Qy 1518 AGCCAG 1577
Db 1501 AGCCAG 1560
Qy 1578 AGCTGCCACCCCTGAGCCCGCTATGGCCAGCCGAGACAGACAGCCCGAGAGGGCGCCAG 1637
Db 1561 AGCTGCCACCCCTGAGCCCGCTATGGCCAGCCGAGACAGACAGCCCGAGAGGGCGCCAG 1620
Qy 1638 AGGCAAGGCTCCACCCCTTATGAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1697
Db 1621 AGGCAAGGCTCCACCCCTTATGAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Qy 1698 AAGGAG 1757
Db 1681 AAGGAG 1740
Qy 1758 GTGGAG 1817
Db 1741 GTGGAG 1800
Qy 1818 TCCCCCAATGCCCCCAATCCAGTGGGGGCTAATCTAGGGGTCACGGGAGAGAGTCTCGT 1877
Db 1801 TCCCCCAATGCCCCCAATCCAGTGGGGGCTAATCTAGGGGTCACGGGAGAGAGTCTCGT 1860
Qy 1878 CTCTGTGTGTATGT 1937
Db 1861 CTCTGTGTGTATGT 1920
Qy 1938 GCATGATTCCTGT 1997
Db 1921 GCATGATTCCTGT 1980
Qy 1998 GGAATGCTGTCTAGAGATCTCAGGGGGGCTCTGTCTCTCTTCCCTTCCCTTCTGTGCT 2057
Db 1981 GGAATGCTGTCTAGAGATCTCAGGGGGGCTCTGTCTCTCTTCCCTTCCCTTCTGTGCT 2040
Qy 2058 CACCAATCCCCCTAGGAGGCGCTGCAAGGTCCCAACTCTCCAGGCGCTTAACTTGGGCG 2117
Db 2041 CACCAATCCCCCTAGGAGGCGCTGCAAGGTCCCAACTCTCCAGGCGCTTAACTTGGGCG 2100
Qy 2118 GCTTGGCTTGAAGTGTCTTCCAGCGAGGCGCTGTACGCGGTCTTGAAGCTCTTGAC 2177
Db 2101 GCTTGGCTTGAAGTGTCTTCCAGCGAGGCGCTGTACGCGGTCTTGAAGCTCTTGAC 2160
Qy 2178 ATGAAGT 2237
Db 2161 ATGAAGT 2220
Qy 2238 GGAATGCAAG 2297
Db 2221 GGAATGCAAG 2280

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QY 2298 GCTCACTAGCTGTGAGAGTCTCTCAGAGTGGAGAGATGATGAGAGGAGAGCTTCC 2357
DB 2281 GCTCACTAGCTGTGAGAGTCTCTCAGAGTGGAGAGATGATGAGAGGAGAGCTTCC 2340
QY 2358 ATTTTGTCTCTCTAGAGACCTGTATATTTGTATATTTCTCTCTCGAGTCTCTGA 2417
DB 2341 ATTTTGTCTCTCTAGAGACCTGTATATTTGTATATTTCTCTCTCGAGTCTCTGA 2400
QY 2418 GTGGGCTGCTCTGCTGACCTGACCTGATGAGCTCTAGAGGAGAGAGAACATTAGGA 2477
DB 2401 GTGGGCTGCTCTGCTGACCTGACCTGATGAGCTCTAGAGGAGAGAGAACATTAGGA 2460
QY 2478 CGTGGCAATAGACCTGGGAGGAGAGAGTACAGCCAGACCCAGTGTCCAGCTTAC 2537
DB 2461 CGTGGCAATAGACCTGGGAGGAGAGAGTACAGCCAGACCCAGTGTCCAGCTTAC 2520
QY 2538 TGGGTCTCTACCTGGGAGGAGAGAGGAGGAGTACCTCTGCTCTCTAGATGAGC 2597
DB 2521 TGGGTCTCTACCTGGGAGGAGAGAGGAGGAGGAGTACCTCTGCTCTCTAGATGAGC 2580
QY 2598 CACCTCTCAATCTCAGCCAGACAGTCTCTCCACCCCTAGGAGGAGTGTGATGAGCA 2657
DB 2581 CACCTCTCAATCTCAGCCAGACAGTCTCTCCACCCCTAGGAGGAGTGTGATGAGCA 2640
QY 2658 TAACTCATATCTGATTTGAGAGTTTGCCCTTTACAGGAGGAGATTTTCTGCTCAGTTCA 2717
DB 2641 TAACTCATATCTGATTTGAGAGTTTGCCCTTTACAGGAGGAGATTTTCTGCTCAGTTCA 2700
QY 2718 ACAATGAAATGAGAGAGACCTCTCTTCTACAGCTCATCTTATCAGAGGAGGAGGAG 2777
DB 2701 ACAATGAAATGAGAGAGACCTCTCTTCTTCTACAGCTCATCTTATCAGAGGAGGAGGAG 2760
QY 2778 CCTCAGAGCCAGATTGAGTTGCTTTTCTGAGATGAGAGAGTAACTCCCACT 2837
DB 2761 CCTCAGAGCCAGATTGAGTTGCTTTTCTGAGATGAGAGAGTAACTCCCACT 2820
QY 2838 TTCTTGAGGAGAGGCTCTGACAGAGTGCCTTTGTACAGACCTTACACAGCTGATAGAGC 2897
DB 2821 TTCTTGAGGAGAGGCTCTGACAGAGTGCCTTTGTACAGACCTTACACAGCTGATAGAGC 2880
QY 2898 AGCCACATTTGCTCTGCGCCCTTGTCTGCGACCTCGTGTGTGTCTGCTCTCTCTGCA 2957
DB 2881 AGCCACATTTGCTCTGCGCCCTTGTCTGCGACCTCGTGTGTGTCTGCTCTCTCTGCA 2940
QY 2958 TGCTGTGGGCTGCTCTGAGTGTGAGAGTGGGTTAACTGTGCTCTGCTGAGC 3017
DB 2941 TGCTGTGGGCTGCTCTGAGTGTGAGAGTGGGTTAACTGTGCTCTGCTGAGC 3000
QY 3018 TGGCAATTAACATCACCTGTC 3039
DB 3001 TGGCAATTAACATCACCTGTC 3022

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RESULT 3
AADI8832
ID AADI8832 standard; cDNA; 3017 BP.

AC AADI8832;
XX
XX 18-DEC-2001 (first entry)
XX
XX Human kinase (PKIN)-17 cDNA.
XX
XX Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout;
XX
XX cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome;
XX
XX AIDS; Addison's disease; microbial infection; inflammation; osteoporosis;
XX
XX atherosclerosis; cardiovascular disease; myocardial infarction; anaemia;
XX
XX myasthenia gravis; cirrhosis; cataract; growth and development disorder;
XX
XX seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder;
XX
XX lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease;
XX
XX obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular;
XX
XX antimicrobial; cytostatic; antiinflammatory; asthma; ss.

```

OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 180..1685
FT /*tag=a
FT /*product="Human PKIN-17 protein"
XX
XX MO200181555-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001MO-US012992.
XX
XX 20-APR-2000; 2000US-0199021P.
XX
XX 28-APR-2000; 2000US-020026P.
XX
XX 05-MAY-2000; 2000US-020233P.
XX
XX 11-MAY-2000; 2000US-020350P.
XX
XX 18-MAY-2000; 2000US-020556P.
XX
XX 26-MAY-2000; 2000US-020773P.
XX
XX 01-JUN-2000; 2000US-020879P.
XX
XX (INCYTE GENOMICS INC.
XX
XX Yue H, Gandhi AR, Tripathy CM, Kearney L, Griffin JA, Nguyen DB;
XX Bandman O, Lu DM, Lal P, Burford N, Khan FA, Malia NK, Yao MG;
XX Patterson C, Burrill JD, Marcus GA, Zingler KA, Reddon SA, Lu Y;
XX Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR;
XX Walsh RT, Rankumar J, Borowsky ML, Au-Young J, Hillman JL;
XX Gururajan R;
XX
XX WPI; 2001-611740/70.
XX
XX P-PSDB; AAE11783.
XX
XX Human kinases and nucleic acids, useful for preventing diagnosing and
XX treating cancers, inflammation and immune disorders.
XX
XX Claim 5; Page 164-165; 166pp; English.
XX
XX The present invention relates to human kinases (PKIN) and the nucleic
XX acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is
XX used in the prevention, diagnosis and treatment of diseases cancers,
XX adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease,
XX acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies,
XX gout, microbial infections, cardiovascular disease and/or inflammation,
XX myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial
XX infarction, cataract, growth and development disorder, seizure disorder,
XX pulmonary embolism, Gaucher's disease, lipid disorder, lipid storage
XX disease, Pick's disease, Tay-Sachs disease, renal disease and obesity.
XX PKIN may be used to treat disorders associated with decreased PKIN
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of PKIN by expressing inactive proteins or to
XX supplement the patient's own production of PKIN. PKIN nucleic acids may be
XX used to produce the PKIN polypeptide, by inserting the nucleic acids into
XX a host cell and culturing the cell to express the protein. PKIN nucleic
XX acid and its complementary sequences may also be used as DNA probes in
XX diagnostic assays to detect and quantitate the presence of similar
XX nucleic acid sequences in samples and therefore which patients may be in
XX need of restorative therapy. The present sequence is human PKIN-17 cDNA
XX
XX
XX Sequence 3017 BP; 652 A; 849 C; 887 G; 629 T; 0 U; 0 Other;

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Query Match 96.0%; Score 2999.2; DB 4; Length 3017;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 3; Indels 1; Gaps 1;

Matches 3012; Conservative 0;

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QY 34 GCGAAGCGGCTGCGATGCTGAGGTTGCTAGCCGAGCGGCTGATCTGGCGCGGCT 93
DB 2 GCGAAGCGGCTGCGATGCTGAGGTTGCTAGCCGAGCGGCTGATCTGGCGCGGCT 61
QY 94 CTGCCCCGGTGTCTGAGAGCGATTTCTGCGCGCGCTGCCGAGGCTCTGGCGCGCGCT 153
DB 62 CTGCCCCGGTGTCTGAGAGCGATTTCTGCGCGCGCTGCCGAGGCTCTGGCGCGCGCT 121

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QY 154 GAGCCC-GGAGTCACTTCTCCCTGTGACAAACGGCGCTGAGGTTAGAGCTGGCAAT 212
DB 122 GAGCCCGGATCACTTCTCTCTGTGACAAACGGCGCTGAGGTTAGAGCTGGCAAT 181
QY 213 GCGGTTTGGGTGTGTGACTGTGGGCGAGAGAAAGATTAAACCAAGCATCGAGGTGAC 272
DB 182 GCGGTTTGGGTGTGTGACTGTGGGCGAGAGAAAGATTAAACCAAGCATCGAGGTGAC 241
QY 273 TGACAGATATGATTTTGGGACAGGTCAATCAAGCTGAGAGATTGTGAAATCTTCCGGGC 332
DB 242 TGACAGATATGATTTTGGGACAGGTCAATCAAGCTGAGAGATTGTGAAATCTTCCGGGC 301
QY 333 CAAGGACAAAGACAGACAGGAGACTGCAACCTGCAAGAAAGTTCCAGAACGGGAGCGCG 392
DB 302 CAAGGACAAAGACAGACAGGAGACTGCAACCTGCAAGAAAGTTCCAGAACGGGAGCGCG 361
QY 393 CAAGGTCGGAAGAGCTGCGCAAGACGAGATAGGCAATCCCTCAAGATGTGAAAGCATCCCA 452
DB 362 CAAGTGTGGGAAAGCTGCGCAAGACGAGATAGGCAATCCCTCAAGATGTGAAAGCATCCCA 421
QY 453 CATCTTACAGCTGTGTGATGTGTGTGACCCGCAAGAGATCTTTATCTTCTGGAGCT 512
DB 422 CATCTTACAGCTGTGTGATGTGTGTGACCCGCAAGAGATCTTTATCTTCTGGAGCT 481
QY 513 GGCACAGGGGAGGAGGTGTGTGACTGGATCTGTGACCAAGGCTATCTACTCGAGCGAGA 572
DB 482 GGCACAGGGGAGGAGGTGTGTGACTGGATCTGTGACCAAGGCTATCTACTCGAGCGAGA 541
QY 573 CACAAAGCAACGTGTGATACGGCAAGCTCTGAGGCGCTGACCTTATTTGGCACTCACTCAAT 632
DB 542 CACAAAGCAACGTGTGATACGGCAAGCTCTGAGGCGCTGACCTTATTTGGCACTCACTCAAT 601
QY 633 CTGTGACAGAGATCTTCAAGCTGGAAGAACTGTGTTACTTAACAACGGCTGAAGAACTCGAA 692
DB 602 CTGTGACAGAGATCTTCAAGCTGGAAGAACTGTGTTACTTAACAACGGCTGAAGAACTCGAA 661
QY 693 GATTGTCAATCAATGATCTTCAATCTGTGCTAAGCTAAGAAATGGCTCATCAAGAGACCTGTG 752
DB 662 GATTGTCAATCAATGATCTTCAATCTGTGCTAAGCTAAGAAATGGCTCATCAAGAGACCTGTG 721
QY 753 TGGGACCCCCAGATATCTGCCCCAGAGGTGTGATGGCGGCGAGCTGTATGACGCCCTGT 812
DB 722 TGGGACCCCCAGATATCTGCCCCAGAGGTGTGATGGCGGCGAGCTGTATGACGCCCTGT 781
QY 813 GGAAGCTGTGGGCAATTTGAGTCAATATGATCAATCCGTGCTTCAAGGCAATCCACCTTTTA 872
DB 782 GGAAGCTGTGGGCAATTTGAGTCAATATGATCAATCCGTGCTTCAAGGCAATCCACCTTTTA 841
QY 873 TGAGAGGTGTGAAGAAAGATGATTAAGAAACCATGATAAGAACTCTTCCGCAAGATCCT 932
DB 842 TGAGAGGTGTGAAGAAAGATGATTAAGAAACCATGATAAGAACTCTTCCGCAAGATCCT 901
QY 933 GCGTGTGTATGATGATTTGATCTTCCATATTTGGATGATATTTTGGAGCGAGCCAAAGA 992
DB 902 GCGTGTGTATGATGATTTGATCTTCCATATTTGGATGATATTTTGGAGCGAGCCAAAGA 961
QY 993 CCGTGTCAAGGCTGTGATGAGGTGTGAAGAAACCAAGCGGATCACTGCGAGAGAGCGCAT 1052
DB 962 CCGTGTCAAGGCTGTGATGAGGTGTGAAGAAACCAAGCGGATCACTGCGAGAGAGCGCAT 1021
QY 1053 CTCCCATGATGATTTCTGGCAATGCTGCTTCTGTATAAGAACATCAAGATGTGTCTG 1112
DB 1022 CTCCCATGATGATTTCTGGCAATGCTGCTTCTGTATAAGAACATCAAGATGTGTCTG 1081
QY 1113 TGCCCATGATTGAAGAAACTTTTGCAGGGCCAAAGTGAAGAAAGGCTGTCCAGTGAACAC 1172
DB 1082 TGCCCATGATTGAAGAAACTTTTGCAGGGCCAAAGTGAAGAAAGGCTGTCCAGTGAACAC 1141
QY 1173 CCTCATGAAGAACGGCTCCGGGCAACAGACAGTCCAGACGGCTGACGGCCAGTCCGCTTC 1232
DB 1142 CCTCATGAAGAACGGCTCCGGGCAACAGACAGTCCAGACGGCTGACGGCCAGTCCGCTTC 1201
QY 1233 AGCCACAGACACTGTCAACCCCGGGGCTGAGGTTGGGGCCACAGCTGCAAGCTGTGCGAGTGG 1292

DB 1202 AGCCACAGACACTGTCCACCCCGGGGCTGCAAGTGGGGCCACAGCTGTGCGAGTGTG 1261
QY 1293 AGCTACCTGACCCCTTGAGGGGTGATGCTGTGCTGTGCTGCAAGAGTGAATATGTGGCCCC 1352
DB 1262 AGCTACCTGACCCCTTGAGGGGTGATGCTGTGCTGTGCTGCAAGAGTGAATATGTGGCCCC 1321
QY 1353 CGGAGACGTTAGTCCACCCCGAGCCACATATGGAAGTGGCACCCGACCACTGATGGCGAG 1412
DB 1322 CGGAGACGTTAGTCCACCCCGAGCCACATATGGAAGTGGCACCCGACCACTGATGGCGAG 1381
QY 1413 TGTACCCCAAGCCACCGATGGAAGATCACTCAAGCCACTGATGGGAGTGTCAACCCAGT 1472
DB 1382 TGTACCCCAAGCCACCGATGGAAGATCACTCAAGCCACTGATGGGAGTGTCAACCCAGC 1441
QY 1473 CACTGACAGAGAGGCTTACTCAAGCCACTGATGGGAGAGCCACACCAAGAGAGAG 1532
DB 1442 CACTGACAGAGAGGCTTACTCAAGCCACTGATGGGAGAGCCACACCAAGAGAGAG 1501
QY 1533 CACTGTGCCCAACCAACCAAGAGTGCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1592
DB 1502 CACTGTGCCCAACCAACCAAGAGTGCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561
QY 1593 GCGGCTATGGCCCGACCCGAGCAAGCCCAAGAGGCGGCGCAAGGCGAGGCTGCAAC 1652
DB 1562 GCGGCTATGGCCCGACCCGAGCAAGCCCAAGAGGCGGCGCAAGGCGAGGCTGCAAC 1621
QY 1653 CTCTAGTAAAGGGAAGAGGCTGTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1712
DB 1622 CTCTAGTAAAGGGAAGAGGCTGTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1681
QY 1713 CTGAGTAGGAGGCTGTGATGAGGGGGGCAAGGGATGAGGAGAGGTTGAGAGTGAATG 1772
DB 1682 CTGAGTAGGAGGCTGTGATGAGGGGGGCAAGGGATGAGGAGAGGTTGAGAGTGAATG 1741
QY 1773 AGGGGCTTCTCACTGTATCATATAGTCACTGTGATATGCTGCTGCTGCTGCTGCTGCTG 1832
DB 1742 AGGGGCTTCTCACTGTATCATATAGTCACTGTGATATGCTGCTGCTGCTGCTGCTGCTG 1801
QY 1833 CATCCAGATGGGGCATATATGAGGGGTCAAGGGAGAGACAGTCTGTCTGTGTGTATGT 1892
DB 1802 CATCCAGATGGGGCATATATGAGGGGTCAAGGGAGAGACAGTCTGTCTGTGTGTATGT 1861
QY 1893 GTGTGATGTGTGGGCAAGGCTGAGGAGGAGGCGGCGCCAGCCCTGATGATATCTCTTGT 1952
DB 1862 GTGTGATGTGTGGGCAAGGCTGAGGAGGAGGCGGCGCCAGCCCTGATGATATCTCTTGT 1921
QY 1953 GGCCTTTCCTGCTTCTTGTGATGCTTCAAGATTTCTGTCTCTGTGGGATGTGCTTGAAG 2012
DB 1922 GGCCTTTCCTGCTTCTTGTGATGCTTCAAGATTTCTGTCTCTGTGGGATGTGCTTGAAG 1981
QY 2013 GATATCTAAGGGGCTCTGTGCTTCCCTTCCCTTCTGTGCTGCTGCTGCTGCTGCTGCTG 2072
DB 1982 GATATCTAAGGGGCTCTGTGCTTCCCTTCCCTTCCCTTCTGTGCTGCTGCTGCTGCTG 2041
QY 2073 CAGGCTCTGCAAGGTCCCACTCTTCCAGGCTTAACTTGGGCGGCTGCTGCTGCTGCTG 2132
DB 2042 CAGGCTCTGCAAGGTCCCACTCTTCCAGGCTTAACTTGGGCGGCTGCTGCTGCTGCTG 2101
QY 2133 CTGTCTCTCCAGAGGAGCCCTGTCAAGGCTCTTAAGGCTCTCTGCAATGAAGGTGTGCC 2192
DB 2102 CTGTCTCTCCAGAGGAGCCCTGTCAAGGCTCTTAAGGCTCTCTGCAATGAAGGTGTGCC 2161
QY 2193 TGTGTGTGTGGGTGTGCTTGAAGAGCATACAGGCTGTGTATGAAGATGCAAAAAGTGA 2252
DB 2162 TGTGTGTGTGGGTGTGCTTGAAGAGCATACAGGCTGTGTATGAAGATGCAAAAAGTGA 2221
QY 2253 GGGCAGTATGTTTAAGTCAAGACTTGGCACAATGGCTTAAGGATCTGTGCTACTAGCTGTGG 2312
DB 2222 GGGCAGTATGTTTAAGTCAAGACTTGGCACAATGGCTTAAGGATCTGTGCTACTAGCTGTGG 2281
QY 2313 AGTCTCTCAGGAGTGAAGAAATGATGAGAGGAGCAAGACTTCAATTTTGTCTTCTCT 2372


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Db 2282 AGTCTCTCAGAGTGGAGAGATGATGAGAGGAGCAAGCTTCATTTTGTCTTCTCT 2341
Qy 2273 AAGACCCCTGTTATTTGTTATTTTCTGCTTCTCGAGTCTCTGAGTGGGCTGCCCTGTA 2432
Db 2342 AAGACCCCTGTTATTTGTTATTTTCTGCTTCTCGAGTCTCTGAGTGGGCTGCCCTGTA 2401
Qy 2433 CCCTGAACCTCATGAGCTCTTAAGGGAAGAGGAAACAATTAGACCTGGCAATGAGACC 2492
Db 2402 CCCTGAACCTCATGAGCTCTTAAGGGAAGAGGAAACAATTAGACCTGGCAATGAGACC 2461
Qy 2493 TGGCAGGGCAGAGTACAAAGCCAGACCCAGCTGTCCAGCCTTACTGGGCTCTTACCCTG 2552
Db 2462 TGGCAGGGCAGAGTACAAAGCCAGACCCAGCTGTCCAGCCTTACTGGGCTCTTACCCTG 2521
Qy 2553 GGGCAAAACAGGAGGAGGCTGATACCTCTTGTCTTCTTAATGAGCCACCTCTCAATCT 2612
Db 2522 GGGCAAAACAGGAGGAGGCTGATACCTCTTGTCTTCTTAATGAGCCACCTCTCAATCT 2581
Qy 2613 CAGCCCAAGTCTCTTCCACCCCTAGGGGGCTTCTGTCATGAGCAATACCTCATATCTGA 2672
Db 2582 CAGCCCAAGTCTCTTCCACCCCTAGGGGGCTTCTGTCATGAGCAATACCTCATATCTGA 2641
Qy 2673 TTTGAGGTTTCCCTTTACAGGGGAGATTTTCTGCTCAATTCAACATGAATGAGA 2732
Db 2642 TTTGAGGTTTCCCTTTACAGGGGAGATTTTCTGCTCAATTCAACATGAATGAGA 2701
Qy 2733 GGAACCTCCCTTTCTTCAAGCTCACTTCTATCAGAGGCCAGAGTCTCTCAGAGCCACATT 2792
Db 2702 GGAACCTCCCTTTCTTCAAGCTCACTTCTATCAGAGGCCAGAGTCTCTCAGAGCCACATT 2761
Qy 2793 GAGTTGCTTTTCTGGAGATGAGGAAAGGTTAACTCCCAAGTTTCTGAGGGAGGCT 2852
Db 2762 GAGTTGCTTTTCTGGAGATGAGGAAAGGTTAACTCCCAAGTTTCTGAGGGAGGCT 2821
Qy 2853 CCTGACAGTGGCCCTTTTGTGAGACCCCTACCAAGCTGATGAGGAGCAATTTGGTCT 2912
Db 2822 CCTGACAGTGGCCCTTTTGTGAGACCCCTACCAAGCTGATGAGGAGCAATTTGGTCT 2881
Qy 2913 CGCCCTTGTCTGGGACATCCGTTGATCTGACCCCTTCTCCCTGATGCTCTTGGGCTGC 2972
Db 2882 CGCCCTTGTCTGGGACATCCGTTGATCTGACCCCTTCTCCCTGATGCTCTTGGGCTGC 2841
Qy 2973 TCTGGGTGTGAGAGTGGTGGGTTAACTGTGCTCTACTGAACTGGCAATTAACATC 3032
Db 2942 TCTGGGTGTGAGAGTGGTGGGTTAACTGTGCTCTACTGAACTGGCAATTAACATC 3001
Qy 3033 ACCCTGCAAGGCCAA 3048
Db 3002 ACCCTGCAAGGCCAA 3017

RESULT 4
ABX71280
ID ABX71280 standard; cDNA; 2923 BP.
XX AC ABX71280;
XX AC
XX 14-Apr-2003 (first entry)
XX
XX Human signal transduction-associated cDNA from clone DKFzphf2_82e4.
XX
XX Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
XX
XX Homo sapiens.
XX
XX W0200112659-A2.
XX
XX 22-FEB-2001.
XX
XX 18-AUG-2000; 2000WO-IB001496.
XX
XX 18-AUG-1999; 99US-014949P.
XX
XX 28-SEP-1999; 99US-0156503P.
XX
PR
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XX
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
PI Wiemann S;
XX
DR WPI; 2001-327840/34.
DR P-PSDB; ABUS2788.
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
XX different human tissues, useful in recombinant DNA methodologies.
XX
PS Claim 1; Page 352-353; 1095bp; English.
XX
CC This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence encodes a polypeptide
CC described in the disclosure of the invention
XX
SQ Sequence 2923 BP; 644 A; 820 C; 849 G; 610 T; 0 U; 0 Other;

Query Match 90.4%; Score 2824.2; DB 5; Length 2923;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2920; Conservative 0; Mismatches 3; Indels 84; Gaps 1;

Qy 49 ATGCTGAGAGTTCGCTTACCCGAAAGGAGCTGATCTGGGCGCCGCTTCCCGCTGCTC 108
Db 1 ATGCTGAGAGTTCGCTTACCCGAAAGGAGCTGATCTGGGCGCCGCTTCCCGCTGCTC 60
Qy 109 GAGAGGAGATTCTGCGCGCGCTGCCGAGAGCCCTGCGCGCCGCTGAGCCGCGATCACT 168
Db 61 GAGAGGAGATTCTGCGCGCGCTGCCGAGAGCCCTGCGCGCCGCTGAGCCGCGATCACT 120
Qy 169 TCCCTCCTGTGACCAACCGCGCTGCAAGTTAGAGCTTGGCAATGCGCTTGGGTGTG 228
Db 121 TCCCTCCTGTGACCAACCGCGCTGCAAGTTAGAGCTTGGCAATGCGCTTGGGTGTG 180
Qy 229 ACTTGGGCGACAGAAAGATATTAACAGCCATCGAGGTGACTGACATATATATTG 288
Db 181 ACTTGGGCGTGAAGAAAGATATTAACAGCCATCGAGGTGACTGACATATATATTG 240
Qy 289 GAGACAGTCAATCAAGATGAGAGTGTGTAATCTTCCGGGCGCAAGAACAAAGCGCA 348
Db 241 GAGACAGTCAATCAAGATGAGAGTGTGTAATCTTCCGGGCGCAAGAACAAAGCGCA 300
Qy 349 GAGACAGTCAACCTGCAAGAGATTCCAGAAAGCGGAGCGCGCAAGGTGCGAAAGCT 408
Db 301 GAGACAGTCAACCTGCAAGAGATTCCAGAAAGCGGAGCGCGCAAGGTGCGAAAGCT 360
Qy 409 GCCAAGAAAGAGATAGGATCTCTAAGATGTGAAAGATCCCAACATCTACAGTGTG 468
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Qy 468 GATGTGTTGTGACCCGCAAGAGATCTTATCTTCTGAGCTGCGCAAGGAGGAG 528
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Qy 529 GTGTTGACTGAGATCTGGAACGAGGCTACTACCTCGAGGAGACAAAGAAAGTGTGTA 588
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Qy 589 CGGCAAGTCTGAGAGCGGTGCTTATTTGACTCACTCAAGATCTGCAAGAGATCTC 648
Db 541 CGGCAAGTCTGAGAGCGGTGCTTATTTGACTCACTCAAGATCTGCAAGAGATCTC 600
Qy 649 AAGCTGAGAACTGTGTTACTCAACCGGCTGAAGAACTCGAAGATTGTATCATGATGAC 708
Db 601 AAGCTGAGAACTGTGTTACTCAACCGGCTGAAGAACTCGAAGATTGTATCATGATGAC 660
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 QY 1308 TAGAGGTGATGCTGCTGCTGCAAAAGATGATATGTCGCCCCGAGACCGTAACTGC 1367
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RESULT 6
 AAI58144
 ID AAI58144 standard; cDNA; 2840 BP.
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 AC AAI58144;
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 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 347.
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 KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX

PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSB-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 PI WPI; 2001-442253/47.
 DR P-PSDB; AAM38988.
 XX
 PS Claim 1; SEQ ID NO 347; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytoprotective activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression.
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 2840 BP; 619 A; 795 C; 834 G; 592 T; 0 U; 0 Other;
 Query Match 89.3%; Score 2791.2; DB 4; Length 2840;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 345 GCAAGCTGCACACCTGCAGAAAGTCCAGAAAGCGGACCGCCGAAAGTGGGAAAGCTG 404
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QY 1790 CATAGAGTCACTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1849
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QY 1850 ACTAGAGAGTCAAG 1909
Db 1845 ACTAGAGAGTCAAG 1904
QY 1910 GCCAGTGGAG 1969
Db 1905 GCCAGTGGAG 1964
QY 1970 CTAGCTTCAACAGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 2029
Db 1965 CTAGCTTCAACAGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 2024
QY 2030 TGGCTCTCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 2089
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QY 2150 CCTGTGCAAG 2209
Db 2145 CCTGTGCAAG 2204
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QY 2330 GAGAAATGATGAG 2389
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Db 2505 AGCCCAAGACCCAGTGTCCAGGCTTATGAGTCTTACCTTGGGCTCAAAACAGAGAGAGGCT 2564

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QY 2630 CCAACCTTAG 2689
Db 2625 CCAACCTTAG 2684
QY 2690 TACAGAGAGAGATTTTCTGCTCAGTTCAACATGAAATGAAGAGAACTCCCTTTCTA 2749
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Db 2745 CAGCTCACTTCTATCAAG 2804
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RESULT 7
ADB48110
ID ADB48110 standard; cDNA; 2840 BP.
XX ADB48110;
AC
XX
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA SEQ ID NO 20.
XX
XX
KW es; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
XX
PN US2003104529-A1.
XX
XX
PD 05-JUN-2003.
XX
XX
PE 04-JAN-2002; 2002US-00037270.
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XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
XX
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIU/) LIU C.
PA (ASUNDI/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX
XX
DR WPI; 2003-678194/64.
XX
XX
PT New polynucleotide, useful for treating diseases e.g., cancer or
neurodegenerative diseases.
XX
PS Claim 1; SEQ ID NO 20; 99PP; English.
XX
XX
CC The invention relates to a polynucleotide comprising a sequence given in
the specification, or its mature protein-coding portion, or its
complement. The polynucleotide is useful for treating diseases e.g.,
cancer or neurodegenerative diseases and many others listed in the
specification. The present sequence represents a novel human cDNA. Note:
The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
at seqdata.uspto.gov/sequence.html?docid=20030104529.
XX
SQ Sequence 2840 BP; 619 A; 795 C; 834 G; 592 T; 0 U; 0 Other;
Query Match 89.3%; Score 2791.2; DB 8; Length 2840;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 TGCCTGAGGTTCCGTACCCGAAAGGGCTGATCTGGGGCCGGCTGCCCCGGTGTCTG 109
Db 45 TGCCTGAGGTTCCGTACCCGAAAGGGCTGATCTGGGGCCGGCTGCCCCGGTGTCTG 104
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QY 1790 CATAGATCACTGGAGATATGCTTCCTGCTCCCCCATGCCCCCATCCAGTGGGGCAT 1849
Db 1785 CATAGATCACTGGAGATATGCTTCCTGCTCCCCCATGCCCCCATCCAGTGGGGCAT 1844
QY 1850 ACTAGGGGTCAGGGAGAGAGTCTGCTCCTGCTGTATGATGATGATGATGATGATGATG 1909
Db 1845 ACTAGGGGTCAGGGAGAGAGTCTGCTCCTGCTGTATGATGATGATGATGATGATGATG 1904
QY 1910 GCCAGTGGAGGGCCGCGCCAGCCCGCATGATGATTCCTTGTGGCTTTCCTGCTTTG 1969
Db 1905 GCCAGTGGAGGGCCGCGCCAGCCCGCATGATGATTCCTTGTGGCTTTCCTGCTTTG 1964
QY 1970 CTAGCTTACCAAGTTTCTGTTCTTGTGGAGTGTCTCTAGAGATCTCAGGGGGCTCC 2029
Db 1965 CTAGCTTACCAAGTTTCTGTTCTTGTGGAGTGTCTCTAGAGATCTCAGGGGGCTCC 2024
QY 2030 TGGTCTCTCCCTCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 2089
Db 2025 TGGTCTCTCCCTCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 2084
QY 2090 ACACTCTCCAGGCGCTTAACTTGGGCGGCTTGGCTGAGAGCTGTCTCTCAGCGAG 2149
Db 2085 ACACTCTCCAGGCGCTTAACTTGGGCGGCTTGGCTGAGAGCTGTCTCTCAGCGAG 2144
QY 2150 CCTGTACAGCGTCTTAAAGCTCTGACATGAAGGTGTGTGCTGTGTGTGTGTGTGTGTG 2209
Db 2145 CCTGTACAGCGTCTTAAAGCTCTGACATGAAGGTGTGTGCTGTGTGTGTGTGTGTGTG 2204

QY	2210	TCATGAGGACGATTCAGGCTCGTATPAGAGATGCGAAAGGATAGGGCAGTATGTTTAACT	22629
Db	2205	TCTTAGGAGCGAGATCAGGCTGATATAGAGATGCGAAAGGATAGGGCAGTATGTTTAACT	22654
QY	2270	CCAGACTTGGCACAATGCGCTAGGGAATCTGCTCACTAGCTGTGAGGTTCTTCAGAGTGGGA	23239
Db	2265	CCAGACTTGGCACAATGCGCTAGGGAATCTGCTCACTAGCTGTGAGGTTCTTCAGAGTGGGA	23244
QY	2330	GAGAAATAGTATAGGAGGGCAGAAAGCTTCCATTTTGTCCCTTCCTPAAAGCCCTGTATTTGT	23839
Db	2325	GAGAAATAGTATAGGAGGGCAGAAAGCTTCCATTTTGTCCCTTCCTPAAAGCCCTGTATTTGT	23844
QY	2390	GTTATTTTCCTGCTTCCTCCGAGTCCCTGCAAGTGGGCTGCCCTGTACCTCGAATCCTCATGAGC	24439
Db	2385	GTTATTTTCCTGCTTCCTCCGAGTCCCTGCAAGTGGGCTGCCCTGTACCTCGAATCCTCATGAGC	24444
QY	2450	CTCTPAAAGGAAAGGAGGAAACAATTATGAGCGTGGCAATGAGACTCTGGCAGGGCAGAGTACA	25039
Db	2445	CTCTPAAAGGAAAGGAGGAAACAATTATGAGCGTGGCAATGAGACTCTGGCAGGGCAGAGTACA	25044
QY	2510	AGCCCAAGACCCCAATGTCGCCAGCCCTTACCTGGGTCCTTACCCTGGGCCCCAAACAGGGAAGGCG	25639
Db	2505	AGCCCAAGACCCCAATGTCGCCAGCCCTTACCTGGGTCCTTACCCTGGGCCCCAAACAGGGAAGGCG	25644
QY	2570	TGATTAACCTCTTGTCTCTTCCAGTATGCCCACCTCTCAATCTGACGCCCAAGATCTCTCT	26239
Db	2565	TGATTAACCTCTTGTCTCTTCCAGTATGCCCACCTCTCAATCTGACGCCCAAGATCTCTCT	26244
QY	2630	CCAACTTAAGGGGGCTGTGCTGATAGGCATAACTCATATCTGATTTTGGAGGTTTGCCCTT	26839
Db	2625	CCAACTTAAGGGGGCTGTGCTGATAGGCATAACTCATATCTGATTTTGGAGGTTTGCCCTT	26844
QY	2690	TACAGGGGCAATTTTCTGCTCAGTTCACACATGAAATGAGAGGAACTCCCTCTTTCTTA	27439
Db	2685	TACAGGGGCAATTTTCTGCTCAGTTCACACATGAAATGAGAGGAACTCCCTCTTTCTTA	27444
QY	2750	CAGCTCACTTCTATCAGAGGCCCAAGTGCCTCAGAGCCACAATTGAGTTGCTTTTCTGGG	28039
Db	2745	CAGCTCACTTCTATCAGAGGCCCAAGTGCCTCAGAGCCACAATTGAGTTGCTTTTCTGGG	28044
QY	2810	ATGAGGAATGAGGTTAACTCCCAAGTTTCTGTAG	2845
Db	2805	ATGAGGAATGAGGTTAACTCCCAAGTTTCTGTAG	2840

RESULT	8
AAFP30481	
ID	AAFP30481 standard; cDNA; 2897 BP.
XX	
XX	AAFP30481;
XX	
DT	29-MAY-2001 (first entry)
XX	
DE	Human protein phosphatase and kinase protein-6 cDNA 1385073CB1.
XX	
KW	Protein phosphatase and kinase protein; PPHKP-6; human;
KW	gastrointestinal disorder; immune system disorder; neurological
KW	cell proliferative disorder; cancer; diagnosis; therapy; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	149..1561
FT	/*tag= a
FT	326..385
FT	/*tag= b
FT	/note= "unique fragment"
FT	1298..1357
FT	/*tag= c
FT	/note= "unique fragment"
XX	
PN	W0200120004-A2.

PX	PD	22-MAR-2001.
PX	PF	14-SEP-2000; 2000WO-US025515.
PX	PR	15-SEP-1999; 99US-0154141P.
PX	PA	(INCY-) INCYTE GENOMICS INC.
XX	PI	Yue H, Tang YT, Bandman O, Hillman JL, Baughn WF, Azimzai Y;
XX	PT	Lu DM;
DR	NR	WFI; 2001-244811/25.
DR	P-P	P-PSDB; AAB20327.
XX	PT	Newel human protein phosphatase and kinase proteins for diagnosis,
XX	PT	treatment and prevention of gastrointestinal, immune system, neurological
XX	PT	and cell proliferative disorders.
PS	XX	Claim 5; Page 99; 103pp; English.
CC	XX	The present sequence is that of cDNA encoding novel human protein
CC	XX	phosphatase and kinase protein PPHK-6 (see AAB20327). The cDNA was
CC	XX	initially identified in Incyte Clone ID No. 1385073CB1, from a brain
CC	XX	tumour tissue library. Tissues that express PPHK-6 (as a fraction of
CC	XX	total tissues expressing PPHK-6) include nervous (0.885) and tissues
CC	XX	developmental (0.077). Diseases or conditions associated with tissues
CC	XX	expressing PPHK-6 (as a fraction of total tissues expressing PPHK-6)
CC	XX	include inflammation or trauma (0.384), neurological (0.231) and cancer
CC	XX	(0.192). The encoded protein shows homology to rat calmodulin-binding
CC	XX	protein. The invention provides human PPHK-1 to -11 polypeptides (see
CC	XX	AAB20322-32) and polynucleotides (see AAf30476-86). It also provides
CC	XX	expression vectors, host cells, antibodies, agonists and antagonists, as
CC	XX	well as methods for diagnosing, treating or preventing disorders
CC	XX	associated with expression of PPHK, including gastrointestinal
CC	XX	disorders, immune system disorders, neurological disorders and cell
CC	XX	proliferative disorders, including cancer
XX	SQ	Sequence 2897 BP; 636 A; 816 C; 838 G; 607 T; 0 U; 0 Other;
Query Match		89.3%; Score 2790.8; DB 4; Length 2897;
Best Local Similarity		96.8%; Pred. No. 0;
Matches 2895; Conservative		0; Mismatches 2; Indels 93; Gaps 1
OY	63	CTAGCGGAAGCGGCTGCATCTGGCGCGCGTGTGCCCGCGTGTCGAGCGGATTCTGC 122
Db	1	CTAGCGGAAGCGGCTGCATCTGGCGCGCGTGTGCCCGCGTGTCGAGCGGATTCTGC 60
OY	123	CGCGCGTCCC GGAGACCTT CGAGCGCCCGCTGAGCGCCCGCATCTTCTCCTGTGACC 182
Db	61	CGCGCGTCCCCGGAACCTT CGAGCGCCCGCTGAGCCCGCGCATCTTCTCCTGTGACC 120
OY	183	AACCGCGGTGAGGTTGAGCGTGGCAATCCGTTGGTGGTGACTCTGGCGGACA 242
Db	121	AACCGCGGTGAGGTTGAGCGTGGCAATCCGTTGGTGGTGACTCTGGCGGACA 180
OY	243	GAGAAGCTTAACACGACCATCGAGGTGACTGACAGATATGATTGGGACAGGTCTCAA 302
Db	181	GAGAAGCTTAACACGACCATCGAGGTGACTGACAGATATGATTGGGACAGGTCTCAA 240
OY	303	GACTGAGAGTTTTGTGAATCTTCCGGGCCAAGACAAACGACAGGACAGTGCAC 362
Db	241	GACTGAGAGTTTTGTGAATCTTCCGGGCCAAGACAAACGACAGGACAGTGCAC 300
OY	363	CTGCAAGAAGTTCAGAAAGCGGAGCGCCGAAAGTGTGCGAAAGAGAGAT 422
Db	301	CTGCAAGAAGTTCAGAAAGCGGAGCGCCGAAAGTGTGCGAAAGAGAGAT 360
OY	423	AGGCATCTCAAGATGAGTAGACATCCCAACATCTCAAGCTGGTGAATGTGTTGTGAC 482
Db	361	AGGCATCTCAAGATGAGTAGACATCCCAACATCTCAAGCTGGTGAATGTGTTGTGAC 420
OY	483	CCCCAAGAAGTATTATCTCTGAGCTGGCCAAGGAGGAGGTGTTGATGGAT 542

Db	421	CCGCAAGGAGTACTTATCTTCTCTGAACTGGCCACGGGAGAGGAGGTTTGACTGGAT	480
QY	543	CTTGGACCAAGGAGCTACTACTCGGAGCGAGACAACAAGCAAGTGATACGGACAGTCTTGA	602
Db	481	CTGGACCAAGGAGCTACTACTCGGAGCGAGACAACAAGCAAGTGATACGGACAGTCTTGA	540
QY	603	GGCGGTGGCTTATTTTGACTCACTCAAAATGTGTGACAGGAATCTCAAGCTTGGAGAACTT	662
Db	541	GGCGGTGGCTTATTTTGACTCACTCAAAATGTGTGACAGGAATCTCAAGCTTGGAGAACTT	600
QY	663	GGTTTACTACAAACGGGTGAAGAACTGGAAGTTGTCTCATGTGACTTCCATCTGGCTTAA	722
Db	601	GGTTTACTACAAACGGGTGAAGAACTGGAAGTTGTCTCATGTGACTTCCATCTGGCTTAA	660
QY	723	GCTAGAAAATGGCTCATCAAGAGACCCCTGTGGGACCCCGAGTATCTGGCCCGCAGAGST	782
Db	661	GCTAGAAAATGGCTCATCAAGAGACCCCTGTGGGACCCCGAGTATCTGGCCCGCAGAGST	720
QY	783	GGTAGCCCGGACGCGGTATGGAACGCTCTGTGGACTGTGGGCCATTTGGAGTCAATGTGA	842
Db	721	GGTAGCCCGGACGCGGTATGGAACGCTCTGTGGACTGTGGGCCATTTGGAGTCAATGTGA	780
QY	843	CATCCTGCTTTCAGGCAATTCACCTTTTCTATGAGAGGTGGAGAAAGATGATTTATGAGA	902
Db	781	CATCCTGCTTTCAGGCAACCCACCTTTTATAGAGAGGTGGAGAAAGATGATTTATGAGA	840
QY	903	CCATGATTAAGATCTCTTCGCGAAGATCCTGGCTGTGACTATGAGTTTGACTCTCCATA	962
Db	841	CCATGATTAAGATCTCTTCGCGAAGATCCTGGCTGTGACTATGAGTTTGACTCTCCATA	900
QY	963	TTGGGATGATATTTTCGACGAGCAGCCAAAGACTGTGTCACAAGGCTGATGGAAGTGAAGCA	1022
Db	901	TTGGGATGATATTTTCGACGAGCAGCCAAAGACTGTGTCACAAGGCTGATGGAAGTGAAGCA	960
QY	1023	AGACCAAGGGATCACTGTCGAGAAAGGCCATCTCCATAGTGAATTTCTGGCAATGCTGC	1082
Db	961	AGACCAAGGGATCACTGTCGAGAAAGGCCATCTCCATAGTGAATTTCTGGCAATGCTGC	1020
QY	1083	TTCTGATTAAGAACTCAAGAGATGGTGTGTGGCCGACATTAAGAAAGCTTTGGCAGAGGC	1142
Db	1021	TTCTGATTAAGAACTCAAGAGATGGTGTGTGGCCGACATTAAGAAAGCTTTGGCAGAGGC	1080
QY	1143	CAAGTGAAGAAGGCTGTCCAGATGACACCTCATGAAACGGCTCCGGGACACAGAGCA	1202
Db	1081	CAAGTGAAGAAGGCTGTCCAGATGACACCTCATGAAACGGCTCCGGGACACAGAGCA	1140
QY	1203	GTCCAGACGGCTGACGCCAGTGGGCTTCAGCCACAGACACTGCGACCCCGGGGCTGC	1262
Db	1141	GTCCAGACGGCTGACGCCAGTGGGCTTCAGCCACAGACACTGCGACCCCGGGGCT--	1198
QY	1263	AGGTGGGGCCACAGTGCAGCTGCGAGTGAAGTACTCAAGCCCTTAGAGGTGATGCTGC	1322
Db	1199	-----	1198
QY	1323	TCGTGTGCAAGAAGTGAATATGTGGCCCCCGCAGACCGTATGTGCAACCCAGCCACAGA	1382
Db	1199	-----GAGACCTGTATGTGCAACCCAGCCACAGA	1227
QY	1383	TGGAAGTGCACCCCGACCACTGATGGCAGTGTCAACCCAGCCACCGATGGAAGCATAC	1442
Db	1228	TGGAAGTGCACCCCGACCACTGATGGCAGTGTCAACCCAGCCACCGATGGAAGCATAC	1287
QY	1443	TTCCAGCACTGATGGGAGTGTCAACCCAGTCACTGACAGAGCGCTACTCCAGCCACTGA	1502
Db	1288	TTCCAGCACTGATGGGAGTGTCAACCCAGCACTGACAGAGCGCTACTCCAGCCACTGA	1347
QY	1503	TGGGAGAACCCACACGACCAAGAAAGAGCACTGTGCCACCAACCCAAAGAGTGCAT	1562
Db	1348	TGGGAGAACCCACACGACCAAGAAAGAGCACTGTGTGCCACCAACCAAGAGTGCAT	1407
QY	1563	GCTGGCCACCAAGGAGCTGCGACCCCTGAGCCGGCTTATGGCCACAGCCGAGCAGCACGCT	1622

[illegible]

QY 2703 TTCTGCTCAGTTCACAAATGAAAGAGAACTCCCTCTTTCTACAGCTCACTTCTA 2762
DB 2548 TTCTGCTCAGTTCACAAATGAAAGAGAACTCCCTCTTTCTACAGCTCACTTCTA 2607
QY 2763 TCAGAGCCCAAGTGTCTCAAGCCCAATTGATGCTTTTCTGGATGAGAAATGAG 2822
DB 2608 TCAGAGCCCAAGTGTCTCAAGCCCAATTGATGCTTTTCTGGATGAGAAATGAG 2667
QY 2823 GTTAAATCCCAAGTGTCTCAAGCCCAATTGATGCTTTTCTGGATGAGAAATGAG 2882
DB 2668 GTTAAATCCCAAGTGTCTCAAGCCCAATTGATGCTTTTCTGGATGAGAAATGAG 2727
QY 2883 ACAGCCTGATGAGGAGCCCAATTGATGCTTTTCTGGATGAGAAATGAG 2942
DB 2728 ACAGCCTGATGAGGAGCCCAATTGATGCTTTTCTGGATGAGAAATGAG 2787
QY 2943 GCCCTTCTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3002
DB 2788 GCCCTTCTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2847
QY 3003 TGTGCTCTGATGAGCCTGCAATTAATCAATCACCCTGCAAGCCCAAAAAA 3052
DB 2848 TGTGCTCTGATGAGCCTGCAATTAATCAATCACCCTGCAAGCCCAAAAAA 2897

RESULT 9
AA158143
ID AA158143 standard; cDNA, 2747 BP.

AC AA158143;

DT 22-OCT-2001 (first entry)

DE Human polynucleotide SEQ ID NO 346.

Human; neurotrophic; immunosuppressant; cyostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokine; thrombolytic; drug screening; arthritis; inflammation;
leukaemia; ss.

OS Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US034263.

PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;

DR WPI, 2001-442253/47.
DR P-FSD; AAM38987.

PT Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.

PS Claim 1, SEQ ID NO 346; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AA38642-AA42213) with neurotrophic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 2747 BP; 602 A; 769 C; 801 G; 575 T; 0 U; 0 Other;

Query Match 83.1%; Score 2595.2; DB 4; Length 2747;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 2700; Conservative 0; Mismatches 3; Indels 93; Gaps 1;

QY 50 TGCTGAGGTTCCGCTAGCCGAGAGCCGCTGATGCGCGGCTGCGCCCGCTGCTCG 109
DB 45 TGCTGAGGTTCCGCTAGCCGAGAGCCGCTGATGCGCGGCTGCGCCCGCTGCTCG 104

QY 110 GAGCGATTCTGCCCGCGCTGCCCGAGCCCTGCGCGCCCGCTGAGCCCGCATCTT 169
DB 105 GAGCGATTCTGCCCGCGCTGCCCGAGCCCTGCGCGCCCGCTGAGCCCGCATCTT 164

QY 170 CCTCCCTGTAGCCACCGCGCTGAGGTTAGAGCCTGCGAAAGCCGTTGGGTGTGTGA 229
DB 165 CCTCCCTGTAGCCACCGCGCTGAGGTTAGAGCCTGCGAAAGCCGTTGGGTGTGTGA 224

QY 230 CTCTGGGCGACAAAGAACTATACAGCCATCGAGGAGTGAATGATGATTTGG 289
DB 225 CTCTGGGCGACAAAGAACTATACAGCCATCGAGGAGTGAATGATGATTTGG 284

QY 290 GACAGGTATCAAGACTGAGAGTTTGTAAATCTTCCGGGCAAGACAAAGACAG 349
DB 285 GACAGGTATCAAGACTGAGAGTTTGTAAATCTTCCGGGCAAGACAAAGACAG 344

QY 350 GCAAGCTGCACACTGCAAGAAATTCAGAAAGCGGAGCGCCGCAAGGTGCGAAAGCTG 409
DB 345 GCAAGCTGCACACTGCAAGAAATTCAGAAAGCGGAGCGCCGCAAGGTGCGAAAGCTG 404

QY 410 CCAAGAAAGATAGAGGATCTCAAGATGATGAGATCCCAATCTTACAGCTGTGG 469
DB 405 CCAAGAAAGATAGAGGATCTCAAGATGATGAGATCCCAATCTTACAGCTGTGG 464

QY 470 ATGTGTTGTGACCCGCAAGAGTACTTATCTTCTGAGCTGCGCAACGGGAGGAGG 529
DB 465 ATGTGTTGTGACCCGCAAGAGTACTTATCTTCTGAGCTGCGCAACGGGAGGAGG 524

QY 530 TGTGTAAGTGAATCTGAGCAAGGCTACTACTGAGAGCAACAAAGCAAGTGTGTAC 589
DB 525 TGTGTAAGTGAATCTGAGCAAGGCTACTACTGAGAGCAACAAAGCAAGTGTGTAC 584

QY 590 GCGAAGTCTGAGAGCCGCTGATTTGATCACTCAAGATCTGCAAGGAATCTCA 649
DB 585 GCGAAGTCTGAGAGCCGCTGATTTGATCACTCAAGATCTGCAAGGAATCTCA 644

QY 650 AGCTGAGAACTGGTATTATACACCGGCTGAAGACTGGAAGATGTGATGAGTACT 709
DB 645 AGCTGAGAACTGGTATTATACACCGGCTGAAGACTGGAAGATGTGATGAGTACT 704

QY 710 TCCATCTGAGTAAAGTAAATGAGCCTCATCAAGAGCCCTGTGAGACCCCGAGTATC 769
DB 705 TCCATCTGAGTAAAGTAAATGAGCCTCATCAAGAGCCCTGTGAGACCCCGAGTATC 764
QY 770 TGCCCCAGAGGTGTAGGCGCGGAGGATGTAGAGCCCTGTGAGTGTGAGCCATTG 829

Db	765	TGGCCCCAGAGSTGGTAGCCCGGACGGGTATGAGCGCCGTGTGACCTGCTGGGCANTTG	824
Qy	830	GAGTCATATATGACATCCTGCTTTCAAGCAATCCACTTTTCTATGAGAGGTGAAAG	889
Db	825	GAGTCATATATGACATCCTGCTTTCAAGCAATCCACTTTTCTATGAGAGGTGAAAG	884
Qy	890	ATGATTTATGAGAACCATATGAAGATCTCTCCGGAATACTCTGGCTGTGTACTATGCT	949
Db	885	ATGATTTATGAGAACCATATGAAGATCTCTTCCGGAATCTGTGCTGTGTACTATGCT	944
Qy	950	TTGACTCTCCATATTGGATGATATTTTGGCAGGCAAGCACTGTGTCAAGAGCTGA	1009
Db	945	TTGACTCTCCATATTGGATGATATTTTGGCAGGCAAGCACTGTGTCAAGAGCTGA	1004
Qy	1010	TGAGAGTGGAGCAGACCAAGCCGATCACTGCAGAAAGGCCATCTCCATAGATGATTT	1065
Db	1005	TGAGAGTGGAGCAGACCAAGCCGATCACTGCAGAAAGGCCATCTCCATAGATGATTT	1064
Qy	1070	CTGGCAATGCTGCTCTCTGATTAAGAACATCAAGATGTGTCTGTGCCCAATTAAAGA	1129
Db	1065	CTGGCAATGCTGCTCTCTGATTAAGAACATCAAGATGTGTCTGTGCCCAATTAAAGA	1124
Qy	1130	ACTTGGCAGAGGCCCAAGTGAAGAAAGGCTGTCCGAGTACCAACCTCATGAAAGGGCTCC	1189
Db	1125	ACTTGGCAGAGGCCCAAGTGAAGAAAGGCTGTTCGAGTACCAACCTCATGAAAGGGCTCC	1184
Qy	1190	GGGACCAAGACAGTCCAGCAAGCGCTGCAGCCAGTGGACCTCAAGCCACAGACACTGCCA	1249
Db	1185	GGGACCAAGACAGTCCAGCAAGCGCTGCAGCCAGTGGACCTCAAGCCACAGACACTGCCA	1244
Qy	1250	CCCCCGGGGCTGCAGGTGGGGCCACGCTGCAGCTGCAGTGAAGCTTACCGCCCTGTG	1309
Db	1245	CCCCCGGGGCT-----	1255
Qy	1310	AGGGTATGCTGCTGCTGTGCTGCAAAAGATGATATGTGGCCCCCGGACACCGGTAGTGCA	1369
Db	1256	-----GCAACCGTATGTGCA	1271
Qy	1370	CCCCAGCCACAGATGAGATGACCAACCCAGCCACTGATGAGAGTGTCAACCCAGCACCG	1429
Db	1272	CCCCAGCCACAGATGAGATGACCAACCCAGCCACTGATGAGAGTGTCAACCCAGCACCG	1331
Qy	1430	ATGGAAGCATCACTCCAGCCACTGATGGAGTGTCAACCCAGTCACTGACAGAGCGCTA	1489
Db	1332	ATGGAAGCATCACTCCAGCCACTGATGGAGTGTCAACCCAGTCACTGACAGAGCGCTA	1391
Qy	1490	CTCCAGCCACTGATGGAGAGTCCACCAAGCCACAGAAAGACACTGTGCCACACCC	1549
Db	1392	CTCCAGCCACTGATGGAGATACCAACAGCCACAGAAAGACACTGTGCCACACCC	1451
Qy	1550	AAAGCAGTGCATGTGTGACCAACAGGAGGCTGCCACCCGTGAGCGGCTATGGCCAGC	1609
Db	1452	AAAGCAGTGCATGTGTGACCAACAGGAGGCTGCCACCCGTGAGCGGCTATGGCCAGC	1511
Qy	1610	CGGACAGCACAGCCCCAGAGGGCGCCACAGGCCAGGCTCAACCCCTTAGTAAAGGGAGG	1669
Db	1512	CGGACAGCACAGCCCCAGAGGGCGCCACAGGCCAGGCTCAACCCCTTAGTAAAGGGAGG	1571
Qy	1670	AGGCTGCTGGTTATATGCCAGAGTCTCAAAGGAGAGAGGCCAGCTAGTAGGCAAGCTGG	1729
Db	1572	AGGCTGCTGGTTATATGCCAGAGTCTCAAAGGAGAGAGGCCAGCTAGTAGGCAAGCTGG	1631
Qy	1730	TGAGGGGGGGAGGGGATGGGAGGAGGGGTGGAGAGTGAATGAGGGGCTTCTCACTGTA	1789
Db	1632	TGAGGGGGGGAGGGGATGGGAGGAGGGGTGGAGAGTGAATGAGGGGCTTCTCACTGTA	1691
Qy	1790	CATAGAGTCACTGGCATGATGCCCCCTGCTCCCCCATGCCCCCACTCCCAATGGGGCAT	1849
Db	1692	CATAGAGTCACTGGCATGATGCCCCCTGCTCCCCCATGCCCCCACTCCCAATGGGGCAT	1751
Qy	1850	ACTAGGGGTCACGGGAGACAGTCTCGTCTCTGTGTATGTGTGATGTGTGGCGAG	1909

[illegible]

RESULT 10	
ADB48109	
ID	ADB48109 standard; cDNA; 2747 BP
XX	
AC	ADB48109;
XX	

DT 04-DEC-2003 (first entry)
 XX Novel human cDNA SEQ ID NO 19.
 XX ss; cancer; neurodegenerative disease; human.
 XX Homo sapiens.
 XX US2003104529-A1.
 XX 05-JUN-2003.
 XX 04-JAN-2002; 2002US-00037270.
 XX 21-JAN-2000; 2000US-00488725.
 XX 25-APR-2000; 2000US-00552317.
 XX 19-JUL-2000; 2000US-00620312.
 XX (ZHOU) ZHOU P.
 XX (TANG) TANG Y T.
 XX (LIUC) LIU C.
 XX (ASUN) ASUNDI V.
 XX (DRMA) DRMANAC R T.
 XX Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
 DR WPI; 2003-678194/64.
 XX New polynucleotide, useful for treating diseases e.g., cancer or
 PT neurodegenerative diseases.
 XX Claim 1; SEQ ID NO 19; 99P; English.
 XX The invention relates to a polynucleotide comprising a sequence given in
 CC the specification, or its mature protein-coding portion, or its
 CC complement. The polynucleotide is useful for treating diseases e.g.,
 CC cancer or neurodegenerative diseases and many others listed in the
 CC specification. The present sequence represents a novel human cDNA. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=20030104529.
 XX
 XX Sequence 2747 BP; 602 A; 769 C; 801 G; 575 T; 0 U; 0 Other;
 SQ
 Query Match 83.1%; Score 2595.2; DB 8; Length 2747;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 2700; Conservative 0; Mismatches 3; Indels 93; Gaps 1;

Db
 405 CCAAGAAAGAGATGAGATCTTCAAGTGGTGAAGATCCCAATCTCAAGTGTGG 464
 470 ATGTGTTTGTGACCCGCAAGAGACTTATCTTCTGTGAGTGGCCACGGGAGGAG 529
 465 ATGTGTTTGTGACCCGCAAGAGACTTATCTTCTGTGAGTGGCCACGGGAGGAG 524
 530 TGTGTTGACTGATCTTGAACCAAGGCTTACTCTGAGGAGACACAAGACGTGTAC 589
 525 TGTGTTGACTGATCTTGAACCAAGGCTTACTCTGAGGAGACACAAGACGTGTAC 584
 590 GGCAGTCTGTGAGAGCCGTGGCCCTATTGCACTCAAGATCTGACAGAGATCTCA 649
 585 GGCAGTCTGTGAGAGCCGTGGCCCTATTGCACTCAAGATCTGACAGAGATCTCA 644
 650 AGCTGAGAACTGTGTTTACTCAACACCGCTGAAGAACTGAAATTTGATCATGACT 709
 645 AGCTGAGAACTGTGTTTACTCAACACCGCTGAAGAACTGAAATTTGATCATGACT 704
 710 TCCATCTGTGCTAAGCTAAGAAATGACCTCATCAAGACCTGTGGACCCCGAGTATC 769
 705 TCCATCTGTGCTAAGCTAAGAAATGACCTCATCAAGACCTGTGGACCCCGAGTATC 764
 770 TGGCCCAAGAGTGTGAGCCGCGGCAAGCTGATGAGACCCCTGTGATCTGTGGCCATTG 829
 765 TGGCCCAAGAGTGTGAGCCGCGGCAAGCTGATGAGACCCCTGTGATCTGTGGCCATTG 824
 830 GAGTCATCATGATATCATCTGCTTCAGGCAATCCACTTCTATGAGAGTGGAAAG 889
 825 GAGTCATCATGATATCATCTGCTTCAGGCAATCCACTTCTATGAGAGTGGAAAG 884
 890 ATGATTTAGAAACCATGATTAAGATCTCTCCGCAAGATCTGAGTGTGATGATGAT 949
 885 ATGATTTAGAAACCATGATTAAGATCTCTCTCCGCAAGATCTGAGTGTGATGATGAT 944
 950 TTGACTCTCATATTTGGATGATATTTTGGAGGAGCCAAAGACCTGTGACAAAGGCTGA 1009
 945 TTGACTCTCATATTTGGATGATATTTTGGAGGAGCCAAAGACCTGTGACAAAGGCTGA 1004
 1010 TGGAGTGTGAGCAAGACCAAGGAGTCACTGCAAGAAAGGCCATCTCCCATGAGTGTG 1069
 1005 TGGAGTGTGAGCAAGACCAAGGAGTCACTGCAAGAAAGGCCATCTCCCATGAGTGTG 1064
 1070 CTGGCAATGCTGCTTCTGATTAAGAAATCAAGAGTGTGCTGTGCCAGATTGAAGA 1129
 1065 CTGGCAATGCTGCTTCTGATTAAGAAATCAAGAGTGTGCTGTGCCAGATTGAAGA 1124
 1130 ACTTTGCGAGGCGCAAGTGAAGAAAGCTGTCCAGATGACCACTCTCATGAAAGCGCTCC 1189
 1125 ACTTTGCGAGGCGCAAGTGAAGAAAGCTGTCCAGATGACCACTCTCATGAAAGCGCTCC 1184
 1190 GGGCACCAAGACAGTCCAGACCGCTGAGCCAGTGTGCTTCAAGCAAGACACTGCCA 1249
 1185 GGGCACCAAGACAGTCCAGACCGCTGAGCCAGTGTGCTTCAAGCAAGACACTGCCA 1244
 1250 CCCCCGGGGCTGCAAGTGGGGCCACAGCTGAGTGGAGTGAAGTCAAGCTCAAGCCCTG 1309
 1245 CCCCCGGGGCT----- 1255
 1310 AGGGTATGCTGCTGCTGCTCAAGAGTGAATATGTGGCCCCCGCAGACCGTATGCTCA 1369
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 1370 CCCCAGCCAGATGAGAGTGCACCCCGACCTGATGAGAGTGCACCCCGACCCAG 1429
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 1430 ATGAGAGATCACTTCAGCCACTGATGAGAGTGCACCCCGACCTGATGAGAGTGCAC 1489
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Db	1572	AGGCTGCTGATTATGCCAGGAGTCTCAAAGGAGAGGACGAGCTGATAGGACGCTGG	1631
Qy	1730	TGAGGGGGGGGCAAGGGATGGCGAGAGGGGTGGAGATGTATAGAGGGCTTCTCATGTATA	1789
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Qy	1790	CATAGAGTCACTGGGATGATAGCCCTCGCTCCCCATGGCCCCATATCCCATTTGGGGCATA	1849
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Qy	1850	ACTAGGGGCTCACGGGAGAGAGCTCGATCGTCCCTGTATATGTGTGTGAGTGTGGGAG	1909
Db	1752	ACTAGGGGCTCACGGGAGAGAGCTCGATCGTCCCTGTATATGTGTGTGAGTGTGGGAG	1811
Qy	1910	GCCAGTGGCAGGGCCGGCCCAAGCCCTCGATGATATTCCTTTGAGCTTTTCTGTCTTTTG	1969
Db	1812	GCCAGTGGCAGGGCCGGCCCAAGCCCTCGATGATATTCCTTTGAGCTTTTCTGTCTTTTG	1871
Qy	1970	CTAGCTTACCAAGTTCCTGTTCCTTTGTGGATGCTGCTCTAGGATACTCAGGGGGCTCC	2029
Db	1872	CTAGCTTACCAAGTTCCTGTTCCTTTGTGGATGCTGCTCTAGGATACTCAGGGGGCTCC	1931
Qy	2030	TGCTCTCCTTCCCCCTTCCCTCTTGAGCCACATTCGCCCTTAGAGGACGGCCCGAGGTCCC	2089
Db	1932	TGCTCTCCTTCCCCCTTCCCTCTTGAGCCACATTCGCCCTTAGAGGACGGCCCGAGGTCCC	1991
Qy	2090	AACCTCTCCACGGCCCTTAACTTGGGCGCCCTTGCCCTTAGAGCTGTGCTCCACGAGG	2149
Db	1992	AACCTCTCCACGGCCCTTAACTTGGGCGCCCTTGCCCTTAGAGCTGTGCTCCACGAGG	2051
Qy	2150	CCCTGTCAAGGGCTCTTAGGCTCTCGCATGAAAGGTGTGCTGTGGTGTGTGGGCTGC	2209
Db	2052	CCCTGTCAAGGGCTCTTAGGCTCTCGCATGAAAGGTGTGCTGTGGTGTGTGGGCTGC	2111
Qy	2210	TCTAGAGACAAATACAGGCTGTATATAGAGATGCAGAAAGGTAGGCGAGTATGTTTAACT	2269
Db	2112	TCTAGAGACAAATACAGGCTGTATATAGAGATGCAGAAAGGTAGGCGAGTATGTTTAACT	2171
Qy	2270	CCAAGCTTGGACATATGGCTTAGGGATATCTGCTCACTAGCTGTGAGAGTCTCAGAGATGGA	2329
Db	2172	CCAAGCTTGGACATATGGCTTAGGGATATCTGCTCACTAGCTGTGAGAGTCTCAGAGATGGA	2231
Qy	2330	GAGAAATGATAGAGAGGCGAGAGCTTCATTTTGTCTTCCTTACAGAACCCGTATTTGT	2389
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Qy	2390	GTTATTTTCTGTGCTTTCCGAGTCTCTGCAGTGGGCTGCCCTTATCCCTGAACTCATAGC	2449
Db	2292	GTTATTTTCTGTGCTTTCCGAGTCTCTGCAGTGGGCTGCCCTTATCCCTGAACTCATAGC	2351
Qy	2450	CTCTAAGGGAAGAAGAGAACAATTATAGACGTGTGGCAATATAGACTTGGGACAGGCAAGTACA	2509
Db	2352	CTCTAAGGGAAGAAGAGAACAATTATAGACGTGTGGCAATATAGACTTGGGACAGGCAAGTACA	2411
Qy	2510	AGCCAGCACCACATGTGTCCAGCTTACTTGGGTCTTACCTCTGGGCAAAACAGGAGAGGC	2569
Db	2412	AGCCAGCACCACATGTGTCCAGCTTACTTGGGTCTTACCTCTGGGCAAAACAGGAGAGGC	2471
Qy	2570	TGATATCTCTTGTCTTCTTCTAGATGCCACCTCTCATATCTCAAGCCACAGTCTCT	2629
Db	2472	TGATATCTCTTGTCTTCTTCTAGATGCCACCTCTCATATCTCAAGCCACAGTCTCT	2531

Qy		2630	CCACCCCTAGGGGCGTTTCTGCATGCAATTAATCATTAATCTGAATTGAGGTTTGCCCTT	2689
Dd		2532	CCACCCTTAGGGGCGTTTCTGCATGCAATTAATCATTAATCTGAATTGAGGTTTGCCCTT	25919
Qy		2690	TACAGGGGCAATTTTGTCTCAGTTCAACAATGAATAAAGAAGAACTCCCTCTTTCTA	2749
Dd		2592	TACAGGGGCAATTTTGTCTCAGTTCAACAATGAATAAAGAAGAACTCCCTCTTTCTA	26511
Qy		2750	CAGCTCACTTTCATCAAGAGGCCAGGCGCTCAAGAGCAATTGAATTGCTTTTCTGGG	2809
Dd		2652	CAGCTCACTTTCATCAAGAGGCCAGGCGCTCAAGAGCAACTGAGTTGCTTTTCTGGG	27111
Qy		2810	ATGAGGAAGTAGGGTTAACTCCCCAGTTTCCTAG	2845
Dd		2712	ATGAGGAAGTAGGGTTAACTCCCCAGTTTCCTAG	2747
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RESULT 11				
AAH78261				
ID	AAH78261	standard; cDNA; 2297 BP.		
XX	AAH78261;			
AC				
XX				
DT	26-NOV-2001	(first entry)		
XX				
DE	Nucleotide sequence of human kinase 2504.			
XX				
KW	Human; kinase; 2504; 15977; 14760; cellular proliferative disorder;			
KW	cellular differentiative disorder; neural disorder; immune disorder;			
KW	cardiovascular disorder; liver disorder; skin disorder;			
KW	skeletal muscle disorder; bone metabolism; cardiovascular disorder;			
KX	vital disease; pain; metabolic disorder; blood vessel disorder;			
KM	hepatic disorder; liver disorder; ss.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	154..1659		
FT		/*tag= a		
FT		/product= "kinase"		
FT		/transl_except= {pos: 157..159, aa: Phe}		
XX				
PN	WC000164905-A2.			
XX				
PD	07-SEP-2001.			
XX				
PF	28-FEB-2001; 2001MC-US006525.			
XX				
PR	29-FEB-2000; 2000US-0186061P.			
PA	(MILL-) MILLENNIUM PHARM INC.			
XX				
PI	Olandt PJ, Kapeller-Libermann R, Meyers RA;			
DR	MPJ: 2001-570697/64.			
XX	P-Psdb; AAG67539.			
PT	New protein kinase family polypeptides for treating hematopoietic			
PT	neoplastic disorders, immune disorders, cardiovascular disorders and			
PT	disorders of blood vessels.			
XX				
PS	Claim 2; Fig 1A-B; 145dp; English.			
XX				
CC	The present sequence encodes human kinase 2504. The specification also			
CC	describes kinases 15977 and 14760. The kinase polypeptides and			
CC	polynucleotides are used to treat cellular proliferative or			
CC	differentiative disorders, neural disorders, immune disorders,			
CC	cardiovascular disorders, liver disorders, skin disorders and skeletal			
CC	muscle disorders. They may also be used for controlling disorders			
CC	associated with bone metabolism, cardiovascular disorders, viral			
CC	diseases, pain or metabolic disorders, blood vessel disorders, and			
CC	hepatic or liver disorders			

XX Sequence 2297 BP, 504 A, 643 C, 702 G, 446 T, 0 U, 2 Other;

Query Match 73.1%; Score 2283.4; DB 5; Length 2297;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2284; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 68 CGAAGCGGCTGATCTGGCGCGCGCTGCGCCCGCGTCTCGAGCGGATTCTGCGCGC 127
DB 11 CGAAGCGGCTGATCTGGCGCGCGCTGCGCCCGCGTCTCGAGCGGATTCTGCGCGC 70
QY 128 GTCCCGGAGCGCTGGCGCGCGCTGAGCGCCCGCATCTTCCTCCCTGTGACCAACG 187
DB 71 GTCCCGGAGCGCTGGCGCGCGCTGAGCGCCCGCATCTTCCTCCCTGTGACCAACG 130
QY 188 GCGCTGCAGGTAGAGCGCTGGCAATGCGTTGGGTGTGTGACTGTGGGCGACAAGAGA 247
DB 131 GCGCTGCAGGTAGAGCGCTGGCAATGCGTTGGGTGTGTGACTGTGGGCGACAAGAGA 190
QY 248 ACTATACAGCGCATTCGAGGTGACTGACAGATATGATTTGGAGACAGTCAATCAAGACTG 307
DB 191 ACTATACAGCGCATTCGAGGTGACTGACAGATATGATTTGGAGACAGTCAATCAAGACTG 250
QY 308 AGAAGTTTGTGAAAATCTTCCGGGCGAAGACAGACAGACAGGCAAGCTGCACACTGCA 367
DB 251 AGAAGTTTGTGAAAATCTTCCGGGCGAAGACAGACAGACAGGCAAGCTGCACACTGCA 310
QY 368 AGAAGTTCCAGAAAGCGGAGCGCGCGAGGTGCGGAAAGCTGCGCAAGACAGATAGGCA 427
DB 311 AGAAGTTCCAGAAAGCGGAGCGCGCGAGGTGCGGAAAGCTGCGCAAGACAGATAGGCA 370
QY 428 TCCTCAAGTGTGTGAAGCATCCCAACATCTCTACAGTGTGTGATGTGTTGTGACCGCA 487
DB 371 TCCTCAAGTGTGTGAAGCATCCCAACATCTCTACAGTGTGTGATGTGTTGTGACCGCA 430
QY 488 AGAAGTACTTATCTTCTCGAGCTGCGCACGCGGAGGAGGTGTTTACTGAGACTCTGG 547
DB 431 AGAAGTACTTATCTTCTCGAGCTGCGCACGCGGAGGAGGTGTTTACTGAGACTCTGG 490
QY 548 ACCAGGGCTACTACTCGGAGCGAGACACAGACAGTGTGACGCGAAGTCTGAGGCGCG 607
DB 491 ACCAGGGCTACTACTCGGAGCGAGACACAGACAGTGTGACGCGAAGTCTGAGGCGCG 550
QY 608 TGGCTATTGTGACTCACTCAAGATGTGTCAAGGAACTCAAGCTGAGAACTGTGTT 667
DB 551 TGGCTATTGTGACTCACTCAAGATGTGTCAAGGAACTCAAGCTGAGAACTGTGTT 610
QY 668 ACTACACCGGCGTGAAGACTGGAAGATTGTCACTGACTTCATCGGCTGAAGCTAG 727
DB 611 ACTACACCGGCGTGAAGACTGGAAGATTGTCACTGACTTCATCGGCTGAAGCTAG 670
QY 728 AAAATGCGCTCACTCAAGAGCGCTGTGGAGCCCGCAGATCTGAGCCCGCAGAGTGTAG 787
DB 671 AAAATGCGCTCACTCAAGAGCGCTGTGGAGCCCGCAGATCTGAGCCCGCAGAGTGTAG 730
QY 788 GCGGAGCGGAGTGAAGCGCGCTGTGAGCTGTGGGCAATTGAGTCACTATGATCCTC 847
DB 731 GCGGAGCGGAGTGAAGCGCGCTGTGAGCTGTGGGCAATTGAGTCACTATGATCCTC 790
QY 848 TGGCTTACGCGCATTCACCTTTCTATGAGAGGTGGAAGAGTGTATGAGAACCATG 907
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QY 908 ATAAAGATCTCTCCCGCAAGATCTGAGTGTGATGATGATGATGATGATGATGATG 967
DB 851 ATAAAGATCTCTCTCCCGCAAGATCTGAGTGTGATGATGATGATGATGATGATGATG 910
QY 968 ATGATATTTCGAGGAGCGCAAGACCTGTGTCAAGAGGTGATGAGAGTGTGAGCAAGCC 1027
DB 911 ATGATATTTCGAGGAGCGCAAGACCTGTGTCAAGAGGTGATGAGAGTGTGAGCAAGCC 970
QY 1028 AGCGATCACTGAGAAAGAGCGCATCTCCCATGAGTGTGATTTCTGGCATGTGCTCTCG 1087

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QY 1088 ATAAAGATCAAGAGTGTGTGTGTGCTGCGCAGATTGAAAAGAACTTTTGCAGGGCCCAAGT 1147
DB 1031 ATAAAGATCAAGAGTGTGTGTGTGCTGCGCAGATTGAAAAGAACTTTTGCAGGGCCCAAGT 1090
QY 1148 GGAAGAGGCTGTCCAGTGAACCACTCTATGAAACGCTCCGGGACCCAGAGCACTCA 1207
DB 1091 GGAAGAGGCTGTCCAGTGAACCACTCTATGAAACGCTCCGGGACCCAGAGCACTCA 1150
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DB 1211 GGGCCACAGCTGACGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1270
QY 1328 CTGCAAGAAGTGAATATGTGCTCCCGCAGACCGTATGTGTCACCCACCAAGATGAA 1387
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QY 1388 GTGCCACCCCAAGCACTGATGTGAGTGTCAACCCCAAGCCATGGAAGCATCACTCCAG 1447
DB 1331 GTGCCACCCCAAGCACTGATGTGAGTGTCAACCCCAAGCCATGGAAGCATCACTCCAG 1390
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DB 1391 CCACTGATGGAGTGTCAACCCCAAGTCACTGACAGAGCGCTACTCAGACCACTGATGGA 1450
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QY 1628 AGGCGCCCAAGGCGAGCGCTGCCACCTCTGATGAAAGGGGAGAGGCTGTGATGTGCC 1687
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QY 1868 GCAAGTCTGCTCTGCTGTATGTGTGAGAGTGTGGGAGGCGCATGTGGCAGGGCGCG 1927
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QY 1928 CCCAGCCCTGCAATGATTCCTTGTGCTTTCTGTCTTTTGTGTAGCTTCAACAGTTTCT 1987
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QY 2048 CTTCTTGTGCTCACTTCCCTTAGGAGGCGCTGAGAGTCCCAACATCTCCAGGCGCTTA 2107
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 DB 1141 ATGAAACGGCTCCGGGCAACGAGAGATCCAGACGCGTGCAGCCAGTCCGAGCC 1200
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 QY 1957 TTTCTGTCTTTTGTCTAGCTTCAACAGTTTCTGTCTTGTGGAGTGTCTGTAGGATA 2016
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 DB 1873 -----GTCCTCGTACCT 1887
 QY 2437 GAACCTATGAGCCTCTAAGGGAAGAGAAACAATTAGAGAGTGGCAATGAGACCTGGC 2496
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 DB 2488 TGCAAG 2494

RESULT 13
 AAS27718/c
 ID AAS27718 standard; DNA; 3915 BP.
 AC AAS27718;
 XX
 DT 07-NOV-2001 (first entry)
 DE DNA encoding novel signal transduction pathway protein, Seq ID 1378.
 XX
 XX Neutropenic; cytosolic; dermatological; immunosuppressive; tumour;
 XX anti-inflammatory; anti-HIV; antibacterial; anti-inflammatory; cancer;
 XX immune system disorder rheumatoid arthritis inflammatory condition.

KM organ transplant rejection; infection; hepatitis C; blood disorder;
 KM sickle cell anemia; hyperproliferative disorder; Gaucher's disease;
 KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KM chromosomal abnormality; Down syndrome; ichthemia; renal disorder;
 KM cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KM reproductive system; gastrointestinal; liver disorder; AIDS; ds;
 KM acquired immune deficiency syndrome.

Os Homo sapiens.

PN W0200154733-A1.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001312.

PR	11-JAN-2000	2000US-01790650
PR	04-FEB-2000	2000US-0180628P
PR	24-FEB-2000	2000US-0184664P
PR	02-MAR-2000	2000US-0186350P
PR	16-MAR-2000	2000US-0189674P
PR	17-MAR-2000	2000US-0190076P
PR	18-APR-2000	2000US-0198123P
PR	19-MAY-2000	2000US-0205515P
PR	07-JUN-2000	2000US-0209467P
PR	28-JUN-2000	2000US-0214886P
PR	30-JUL-2000	2000US-0215135P
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PR	14-AUG-2000	2000US-0225758P
PR	16-AUG-2000	2000US-0226279P
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PR	22-AUG-2000	2000US-0226688P
PR	22-AUG-2000	2000US-0227182P
PR	23-AUG-2000	2000US-0227009P
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PR	08-SEP-2000	2000US-023113P
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PR	14-SEP-2000	2000US-0232400P
PR	14-SEP-2000	2000US-0232401P

[illegible]

PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251889P.
PR 08-DEC-2000; 2000US-025190P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM,
XX WPI; 2001-465460/50.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
XX Claim 1; SEQ ID NO 1378; 880bp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders, in wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-
CC AAS27850 represent novel signal transduction pathway protein coding
CC sequences and PCR primers of the invention
XX
XX Sequence 3915 BP; 900 A; 1139 C; 1049 G; 827 T; 0 U; 0 Other;
SQ
Query Match 60.1%; Score 1876.6; DB 4; Length 3915;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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2009 CCTGCTCTCCCAATGCCCCCAATCCAGTGGGAGCATTAAGGGGTCACGGGAGAGCA 1950
Db 1871 GTCTGCTCTCTGTGTATATGTGTAGAGTGTGGGAGGAGCCAGTGGAGGAGGAGGAGG 1930
1949 GTCTGCTCTCTGTGTATATGTGTAGAGTGTGGGAGGAGCCAGTGGAGGAGGAGGAGG 1890
Qy 1931 AGCCCTGAGATGATTCCTGTGGCTTTTGTCTTTGATGATCTTCAACAGATTTCTGT 1990
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Db 1349 ATTAGAGCTGT 1290
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RESULT 14

ADB94521/C
ID ADB94521 standard; DNA; 3915 BP.

XX AC ADB94521;
XX

DT 04-DEC-2003 (first entry)
XX

DE Novel human protein DNA #130.
XX

KM ds; Gene; human; autoimmune disease; Parkinson's disease; silicosis;
KM gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KM immunosuppressive agent; adjuvant; enhance immune response;
KM higher affinity antibody induction;
KM increased serum immunoglobulin concentration.
XX

OS Homo sapiens.
XX

PN US2002168711-A1.
XX

PD 14-NOV-2002.
XX

PF 17-JAN-2001; 2001US-00764868.
XX

PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.

PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
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PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX

PI Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-719985/68.
XX

PT New isolated polypeptide useful for diagnosing and treating
PT immunosuppressive conditions such as autoimmune disease and Parkinson's
PT disease.
XX

PS Disclosure; SEQ ID NO 1378; 345bp; English.
XX

XX The invention relates to an isolated polypeptide. The polypeptide is
CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition in a subject, by determining the presence or
CC amount of expression of the polypeptide in a biological sample and
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition based on the presence or amount of expression of the
CC polypeptide. The polypeptide is also useful for identifying a binding
CC partner to the polypeptide, which involves contacting the polypeptide
CC with a binding partner and determining whether the binding partner
CC effects an activity of the polypeptide. The polypeptide or the nucleic
CC acid encoding the polypeptide is useful for preventing, treating, or
CC ameliorating a medical condition, which involves administering the
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
CC is useful for diagnosing a pathological condition or a susceptibility to
CC a pathological condition in a subject, which involves determining the
CC presence or absence of a mutation in the nucleic acid, and diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC based on the presence or absence of the mutation. The polypeptide, the
CC nucleic acid and an antibody to the polypeptide are useful for treating
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents DNA encoding a novel human protein. Note: The
CC sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format direct from USPRO at
CC seqdata.uspro.gov/sequence.html?docid=20020168711.

XX Sequence 3915 BP; 900 A; 1139 C; 1049 G; 827 T; 0 U; 0 Other;

Query Match 60.1%; Score 1876.6; DB 9; Length 3915;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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DB 1889 AGCCCTGAGATGATTCCTTTGAGCTTTTCTGCTTTTGTAGCTTACACAGTTTCTGT 1830
QY 1991 CCTTGGAGATGCTGCTCTAGAGATATCTAGGGGGCTCCCTGCTCTCTTCCCTTCCCTT 2050
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QY 3011 CTGAACCTGGCAATTAACATCACTCTGCAAGGC 3045
DB 810 CTGAACCTGGCAATTAACATCACTCTGCAAGGC 776
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RESULT 15

ABA95683 standard; DNA; 7542 BP.

ABA95683;

03-APR-2002 (first entry)

DE Human protein kinase gene.
XX Human; protein kinase; enzyme; gene; brain; lung; hippocampus;
KW calmodulin-binding kinase; gene therapy; chromosome 3;
XX single nucleotide polymorphism; SNP; ds.
OS Homo sapiens.

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WO200192492-A2.

PN

06-DEC-2001.

XX

30-MAY-2001; 2001WO-US017327.

XX

30-MAY-2000; 2000US-0207281P.

XX

12-DEC-2000; 2000US-00734030.

XX

(APPL-) APPLERA CORP.

PA

Yan C, Wei M, Ketchum K, Merkulov G, Beasley EM;

PI

WPI; 2002-097770/13.

XX

P-PDB; AAW48279.

DR

New calmodulin-binding kinase peptides and nucleic acid encoding the

PT

peptides, useful as models for developing human therapeutic targets or in

PT

screening for compounds that modulate kinase.

XX

Claim 4; Fig 3; 75pp; English.

PS

The present sequence is a human protein kinase gene. The protein kinase

XX

coding sequence (see ABA95682) is expressed in the brain (both infant and

CC

adult brain), lung and hippocampus. The protein kinase is related to the

CC

calmodulin-binding kinase subfamily. The protein kinase and its coding

CC

sequence can be used as models for the development of human therapeutic

CC

targets, in the identification of human therapeutic agents that modulate

CC

kinase activity in cells and tissues that express the kinase. In

CC

addition, the protein kinase coding sequence can be used for treating a

CC

disorder associated with nucleic acid expression of the kinase gene,

CC

particularly biological and pathological processes that are mediated by

CC

the kinase in cells and tissues that express it, as antisense constructs

CC

to control kinase gene expression in cells, tissues or organisms, and in

CC

gene therapy. The protein kinase gene maps to chromosome 3

XX

Sequence 7542 BP; 1612 A; 1977 C; 2156 G; 1797 T; 0 U; 0 Other;

SO

Query Match 60.1%; Score 1876.6; DB 6; Length 7542;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1890; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1151 AGAAGGCTGTCCGAGTACACCCCTCATGAAACGGCTCCGGGACACAGAGTCCAGCA 1210

DB 3979 AGAAGGCTGTCCGAGTACACCCCTCATGAAACGGCTCCGGGACACAGAGTCCAGCA 4038

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Qy	1331	CAAAAGTGTAAATGTGGCCCCCGCAGACCGTATGTCACCCCAAGCCACAGATGGAAGTG	1390
Db	4159	CAAAAGTGTAAATGTGGCCCCCGCAGACCGTATGTCACCCCAAGCCACAGATGGAAGTG	4218
Qy	1391	CCACCCCAAGCCACTGATGGCAGTGTCAACCCAGCCACCGATGGAAGTATCTCCAGCCA	1450
Db	4219	CCACCCCAAGCCACTGATGGCAGTGTCAACCCAGCCACCGATGGAAGTATCTCCAGCCA	4278
Qy	1451	CTGATGGGAGTGTACCCCAAGTCACTACAGAGAGCGTACTCCAGCCACTGATGGGAGAG	1510
Db	4279	CTGATGGGAGTGTACCCCAAGTCACTACAGAGAGCGTACTCCAGCCACTGATGGGAGAG	4338
Qy	1511	CCACACCAAGCCACAGAAAGAGAGCACTGNGCCACACCCAAAGCAGTGCATGCGCCCA	1570
Db	4339	CCACACCAAGCCACAGAAAGAGAGCACTGNGCCACACCCAAAGCAGTGCATGCGCCCA	4398
Qy	1571	CCAAGGCAAGCTGCCACCCCTGAGCGCGCTATGCGCCACCGGACAGCAAGCCCCAAGG	1630
Db	4399	CCAAGGCAAGCTGCCACCCCTGAGCGCGCTATGCGCCACCGGACAGCAAGCCCCAAGG	4458
Qy	1631	GGCGCAACAGGCCAGGCTTCCACCTCTTATGTAAGGGGAAAGAGCTGCTGTTATGCCAGG	1690
Db	4459	GGCGCAACAGGCCAGGCTTCCACCTCTTATGTAAGGGGAAAGAGCTGCTGTTATGCCAGG	4518
Qy	1691	AGTCTCAAAAGGGAAGAGGCGACGCTGATGAGGCAACCTGTGTAGGGGGGGGCAAGGGAGTGG	1750
Db	4519	AGTCTCAAAAGGGAAGAGGCGACGCTGATGAGGCAACCTGTGTAGGGGGGGGCAAGGGAGTGG	4578
Qy	1751	CAGGAGGGTGGGAGTGGATGAGAGGGGTTCTCATGTACATAAGTCACTGGCATATG	1810
Db	4579	CAGGAGGGTGGGAGTGGATGAGAGGGGTTCTCATGTACATAAGTCACTGGCATATG	4638
Qy	1811	CCCTTGCTCCCCCAATGCCCAACATCCCAATGGGGGCAATACTAGGGGTCACTGGAGAGCA	1870
Db	4639	CCCTTGCTCCCCCAATGCCCAACATCCCAATGGGGGCAATACTAGGGGTCACTGGAGAGCA	4698
Qy	1871	GCTCTGCTCTCTGTGTGTATGTGTGTAGTGTGTAGTGGCAGGCAATGCAAGGGCCGCGCCC	1930
Db	4699	GCTCTGCTCTCTGTGTGTATGTGTGTAGTGTGTAGTGGCAGGCAATGCAAGGGCCGCGCCC	4758
Qy	1931	AGCCCTGCATGATCTCTTGTGGCTTTTCTGTCTTTTGTCTAGCTTCAACCAAGTTTCTGT	1990

Db	5119	GGATACGTGCTCACTAGCTGTGAGAGGTCTCAGAGATGAGAGAAATGATAGAGGGGAGA	5178
QY	2351	AGCTTCACATTTTGTGTCTTCTCTCTTAAGACCTGTGTTATTGTGTTATTTCCTGCCCTTCCGAG	2410
Db	5179	AGCTTCACATTTTGTGTCTTCTCTCTTAAGACCTGTGTTATTGTGTTATTTCCTGCCCTTCCGAG	5238
QY	2411	TCTCGAGTGGGCGCTGCCGTGACCCTGAACCTATGAGCTCTTAAGGGAAAGAGAGACA	2470
Db	5239	TCTCGAGTGGGCGCTGCCGTGACCCTGAACCTATGAGCTCTTAAGGGAAAGAGAGACA	5298
QY	2471	ATTAGGACGTGGCAATGAGACTGTGACGGGACAGTACAAAGCCAGACCCAGTGTCCCA	2530
Db	5299	ATTAGGACGTGGCAATGAGACTGTGACGGGACAGTACAAAGCCAGACCCAGTGTCCCA	5358
QY	2531	GCCTTACTGGGTCTTAACCTGTGGGCCAAACAGGAGAGGCTGATACCTCTTGTCTTCTCT	2590
Db	5359	GCCTTATGGGTCTTAACCATGTGGGCCAAACAGGAGAGGCTGATACCTCTTGTCTTCTCT	5418
QY	2591	AGATGCCACCTCTCTTCAATCTGACGCCCAAGCTCTTCCA-CTTAgggggctTGTGTC	2650
Db	5419	AGATGCCACCTCTCTCAATCTGACGCCCAAGCTCTTCCA-CTTAgggggctTGTGTC	5477
QY	2651	ATGGCAATTAATCTAATATCTGATTTTGGAGTTTGGCCCTTTAAGGGGACATTTTCTGCT	2710
Db	5478	ATGGCAATTAATCTAATATTTGATTTGGAGTTTGGCCCTTTAAGGGGACATTTTCTGCT	5537
QY	2711	CAGTTCAACATGAAATGAGAGAGAACTCCCTCTTTTCAAGCTCACTTCTATCAGAGGC	2770
Db	5538	CAGTTCAACATGAAATGAGAGAGAACTCCCTCTTTTCAAGCTCACTTCTATCAGAGGC	5597
QY	2771	CCAAGTGCCTCAGAGCCACATTGAGTCTTTTCTGGAGTGAAGAGTAGGGTTAACT	2830
Db	5598	CCAAGTGCCTCAGAGCCACATTGAGTCTTTTCTGGAGTGAAGAGTAGGGTTAACT	5657
QY	2831	CCCCAGTTTCTTGAGGAGGAGCTCTGACAGGTGCCCTTTGTCAAGACCTTACACAGCTG	2890
Db	5658	CCCCAGTTTCTTGAGGAGGAGCTCTGACAGGTGCCCTTTGTCAAGACCTTACACAGCTG	5717
QY	2891	GATAGGAGGACCATTTGTCTCTGCGCCCTTGTCTGGGCACTCCGTGATGTCTGTGGCCTTCT	2955
Db	5718	GATAGGAGGACCATTTGTCTCTGCGCCCTTGTCTGGGCACTCCGTGATGTCTGTGGCCTTCT	5777
QY	2951	CCCTGCATGCTGTGGGAGTGTGCTGTGTGTGAAGGCGGTGGTTAACTGTGTGCTTA	3010
Db	5778	CCCTGCATGCTGTGGGAGTGTGCTGTGTGTGAAGGCGGTGGTTAACTGTGTGCTTA	5837
QY	3011	CTGAACCTGGCAATTAACATCACTCTGCAAGGC 3045	
Db	5838	CTGAACCTGGCAATTAACATCACTCTGCAAGGC 5872	

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2291 GGATACTGCTCACTAGCTGTGAGGTCTCAGAGTGGAGGAATGACTTACGAGGCGACA 2350

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